

Qy 3 I I e P h e I I e P h e V a l P h e I I e M e t A l a L e u I I e A r g A l a M e t I I e A r g A l a A s p - S e r S e 22

Ds 2326 GTCTCGTCACTCTCTTCACTTCTCATCCCATCTCGCTCTCGTCTCGTCTGGACTC 2267
QY 22 rGlucLu-LysArgHisArgLysArgLysLysHis--HisArgGlyTyrPheGlnGInt 41
Db 2266 AGAGAGTGGCGCCCATCTTCAGAGAGTCCCATTCATCATCTTCTTCTTCATC 2207
QY 41 yzGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro 56
Db 2206 CTCGCTCGTCACTCTCTTCACTTCTCATCCCATCTCGTCTCGTCTGGACTCG 2160

RESULT 2
US-09-023-655-816/c
; Sequence 816, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; FILE REFERENCE: 24366-20007.00
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023.655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 816:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MYOMNOT01
; CLONE: 781552
; US-09-023-655-816

Alignment Scores:
Pred. No.: 8.79 Length: 3164
Score: 69.50 Matches: 20
Percent Similarity: 56.14% Conservative: 12
Best Local Similarity: 35.09% Mismatches: 22
Query Match: 21.99% Indels: 3
DB: 4 Gaps: 1

US-10-079-754A-10 (1-58) x US-09-023-655-816 (1-3164)

QY 3 ilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaasp-SerSe 22
Db 1224 GTCTCGTCACTCTCTTCACTTCTCATCCCATCTCGTCTCGTCTGGACTC 1165

QY 22 rGlucLu-LysArgHisArgLysArgLysLysHis--HisArgGlyTyrPheGlnGInt 41
Db 1164 AGAGAGTGGCGCCCATCTTCAGAGAGTCCCATTCATCATCTTCTTCTTCATC 1105
QY 41 yzGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrPro 56
Db 1104 CTCGCTCGTCACTCTCTTCACTTCTCATCCCATCTCGTCTCGTCTGGACTCG 1058

RESULT 3
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 5.06e+05 Length: 4403765
Score: 66.00 Matches: 10
Percent Similarity: 58.06% Conservative: 8
Best Local Similarity: 32.26% Mismatches: 13
Query Match: 20.89% Indels: 0
DB: 3 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-103-840A-2 (1-4403765)

QY 18 ArgAlaaspSerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyr 37
Db 1189176 CGTTGCCATACAGCAGCCACCCACCCAGCCGCGCGCGCGCGCGCGCGCG 1189235
QY 38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
Db 1189236 CACCACCGGTACCCACCTTACCGCGCGGTGGCA 1189268

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv


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; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 8.8e+05 Length: 4403765
Score: 63.50 Matches: 17
Percent Similarity: 55.32% Conservative: 9
Best Local Similarity: 36.17% Mismatches: 15
Query Match: 20.09% Indels: 7
DB: Gaps: 1

US-10-079-754A-10 (1-58) x US-09-103-840A-2 (1-4403765)

Qy 18 ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysHisArgGlyTyr 37
Db 3771788 CGTCCCGTTCGTCCCGTACCGCGGACCGCGTTCGCCGCGTACCGCGCGGAAC 3771729

Qy 38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro-----LeuAsnTyr 51
Db 3771728 TACCGGGGACCGCGCTGCCCGCGCG-CCGCCCGACCGCCATTGGACCGCGGTCA 3771670

Qy 52 ProProAlaTyrProPhePro 58
Db 3771669 CCGCGCGGCGCGCGTTCCTCCG 3771649

RESULT 10
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 8.81e+05 Length: 4411529
Score: 63.50 Matches: 17
Percent Similarity: 55.32% Conservative: 9
Best Local Similarity: 36.17% Mismatches: 15
Query Match: 20.09% Indels: 7
DB: Gaps: 1

US-10-079-754A-10 (1-58) x US-09-103-840A-1 (1-4411529)

Qy 18 ArgAlaAspSerSerGluGluLysArgHisArgLysArgLysHisArgGlyTyr 37
Db 3779614 CGTCCCGTTCGTCCCGTACCGCGGACCGCGTTCGCCGCGTACCGCGCGGAAC 3779555
```

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Qy 38 PheGlnGlnTyrGlnProTyrGlnArgTyrPro-----LeuAsnTyr 51
Db 3779554 TACCGCGGACCGCGCTTCGCCCGCGCG-CCGCCCGACCGCCATTGGACCGCGGTCA 3779496

Qy 52 ProProAlaTyrProPhePro 58
Db 3779495 CCGCGGCGCGCGTTCCTCCG 3779475

RESULT 11
US-09-328-352-3819/c
; Sequence 3819, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3819
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3819

Alignment Scores:
Pred. No.: 4.43 Length: 426
Score: 63.00 Matches: 14
Percent Similarity: 51.92% Conservative: 13
Best Local Similarity: 26.92% Mismatches: 18
Query Match: 19.94% Indels: 7
DB: Gaps: 1

US-10-079-754A-10 (1-58) x US-09-328-352-3819 (1-426)

Qy 4 PheIlePheValPheIleMetAlaLeu-IleLeuAlaMetIleArgAlaAspSerSerG1 23
Db 254 TTCTTAAGCGTATTTCTTGCTGTATTATTTCTTAATTCGCTCTTAATGCGGTATTTCTTA 195

Qy 23 uGluLysArgHisArgLysArg-----LysLysHisHisArgGlyTyr 37
Db 194 TTCAGTCTGTCATCAGCATCGCATAGATTTATTGGTACAGTAAATATCATCATAAGTA 135

Qy 37 rPheGlnGlnTyrGlnProTyrGlnArgTyrPro 48
Db 134 TTACGAGCACTATCATCAGTTATCATCAGCATAGACCG 101

RESULT 12
US-09-359-301A-30
; Sequence 30, Application US/09359301A
; Patent No. 6426185
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: della-Cioppa, Guy R.
; APPLICANT: Erwin, Robert L.
; APPLICANT: McGee, David R.
; TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A
; TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSECTING A NUCLEIC ACID SEQUENCE OF
; TITLE OF INVENTION: A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
; FILE REFERENCE: 008010137US04
; CURRENT APPLICATION NUMBER: US/09/359,301A
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-359-301A-30
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Alignment Scores:

Pred. No.: 9.72 Length: 750
Score: 63.00 Matches: 13
Percent Similarity: 58.33% Conservative: 1
Best Local Similarity: 54.17% Mismatches: 10
Query Match: 19.94% Indels: 0
DB: 4 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-359-301A-30 (1-750)

QY 35 ArgGlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAla 54

DB 199 CAGGATATCTCCACACAGGTATCTCCAGCAAGATATCTCCACCGTACGGCCCTCAA 258

QY 55 TyrProPhePro 58

DB 259 TATCTCCACCA 270

RESULT 13

US-08-308-883-1

; Sequence 1, Application US/08308883

; Patent No. 5576300

; GENERAL INFORMATION:

; APPLICANT: Mukerji, P.

; APPLICANT: Prieto, P. A.

; APPLICANT: Seo, A. E.-Y.

; APPLICANT: Baxter, J. H.

; APPLICANT: Cummings, R.D.

; TITLE OF INVENTION: Method for Inhibition of Human Rotavirus Infection.

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lonnie R. Drayer

; ADDRESSEE: Ross Products Division

; ADDRESSEE: Abbott Laboratories

; STREET: 625 Cleveland Avenue

; CITY: Columbus

; STATE: Ohio

; COUNTRY: United States

; ZIP: 43215

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb storage

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh System 7.1

; SOFTWARE: ClarisWorks 1.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/308,883

; FILING DATE: 16-SEP-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: No. 5576300 applicable

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (614) 624-3774

; TELEFAX: (614) 624-3074

; TELEX: No. 5576300e

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 857 base pairs

; TYPE: Nucleic acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; MOLECULE TYPE: cDNA

; DESCRIPTION: Human milk kappa-casein

; HYPOTHETICAL: No

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE: Human

; ORGANISM: Homo sapiens

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE: Adult

; HAPLOTYPE:

; TISSUE TYPE: Mammary gland

; CELL TYPE:

; CELL LINE:

; ORGANELLE:

; IMMEDIATE SOURCE: Human Mammary Gland

; LIBRARY:

; CLONE:

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT:

; MAP POSITION:

; UNITS:

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 45...593

; IDENTIFICATION METHOD: DNA sequencing and restriction analysis

; OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1: is the human

; PUBLICATION INFORMATION:

; AUTHORS: L. Hanson et al

; TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use Thei

; JOURNAL:

; VOLUME:

; ISSUE:

; PAGES:

; DATE:

; DOCUMENT NUMBER: PCT/WO93/15196

; FILING DATE: 25-JAN-1993

; PUBLICATION DATE: 05-AUG-1993

; RELEVANT RESIDUES IN SEQ ID NO:

US-08-308-883-1

Alignment Scores:

Pred. No.: 11.7 Length: 857

Score: 63.00 Matches: 17

Percent Similarity: 50.85% Conservative: 13

Best Local Similarity: 28.81% Mismatches: 25

Query Match: 19.94% Indels: 4

DB: 1 Gaps: 3

US-10-079-754A-10 (1-58) x US-08-308-883-1 (1-857)

QY 1 MetLysIlePheHellePheValPhe---IleMetAlaLeuIleLeuAlaMetIleArgAla 19

DB 45 ATGAAGAGTGTTCCTCTAGTTGTCATGCGCTGGCATTACCCCTGCTGTTTTCGGCTGTG 104

QY 20 AspSerSerGluGluGlyArgHisArgLysArgLysHisArgGlyTyrPheGln 39

DB 105 GAGGTTCAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 164

QY 40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProProAlaTyrProPhe 57

DB 165 AAACACAGCTCCATAT-----GTCCCATGTATTATGTGCGCAAAATAGTATCCTTAT 215

RESULT 14

US-08-730-163-1

; Sequence 1, Application US/08730163

; Patent No. 5712250

; GENERAL INFORMATION:

; APPLICANT: Mukerji, P.

; APPLICANT: Prieto, P. A.

; APPLICANT: Seo, A. E.-Y.

; APPLICANT: Baxter, J. H.

; APPLICANT: Cummings, R.D.

; TITLE OF INVENTION: Product for Inhibition of Human Rotavirus Infection.

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lonnie R. Drayer

; ADDRESSEE: Ross Products Division

; ADDRESSEE: Abbott Laboratories

; STREET: 625 Cleveland Avenue

; CITY: Columbus

; STATE: Ohio

; COUNTRY: United States

; ZIP: 43215

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B) COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh System 7.1 (D) SOFTWARE: ClarisWorks 1.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/730,163
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/308,882
FILING DATE: 16-SEP-1994
TELEPHONE: (614) 624-3774
TELEFAX: (614) 624-3074
TELEX: NO. 5712250e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
DESCRIPTION: Human milk kappa-casein
HYPOTHETICAL: No
ANTI-SENSE:
FRAGMENT TYPE:
ORGANISM: Homo sapiens
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
HAPLOTYPE:
TISSUE TYPE: Mammary gland
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: CDS
LOCATION: 45...593
IDENTIFICATION METHOD: DNA sequencing and restriction analysis
OTHER INFORMATION: The encoded product of nucleotide SEQ ID NO: 1: is the human
PUBLICATION INFORMATION:
AUTHORS: L. Hansson et al
TITLE: DNA Encoding Kappa-Casein, Process for Obtaining the Protein and Use The
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER: PCT/WO93/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
US-08-730-163-1

Alignment Scores:
Pred. No.: 11.7 Length: 857
Score: 63.00 Matches: 17
Percent Similarity: 50.85% Conservative: 13
Best local similarity: 28.81% Mismatches: 25
Query Match: 19.94% Indels: 4
DB: 1 Gaps: 3

US-10-079-754A-10 (1-58) x US-08-730-163-1 (1-857)

Qy 1 MetLysIlePheIlePheValPhe---IleMetAlaLeuIleLeuAlaMetIleArgAla 19
DB 45 ATGAAGAGTTTCTCTAGTGTCAATGCCCTGGCAITTAACCCGCTTTTGGCTGTG 104
Qy 20 AspSerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGln 39

Db 105 GAGGTTCACCAACCAACACAGCAGCATGCCATGAGATGATGAAGACCATTTCTATCAG 164
Qy 40 GlnTyrGlnProTyrGlnArgTyrProLeuAsnTyr---ProPcAlaIaTyrProphe 57
Db 165 AAACAGCTCCATAT-----GTCCCAATGATTATTATGTGCCAAATAGCTATCCTTAT 215
RESULT 15
US-08-256-799-1
Sequence 1, Application US/08256799
Patent No. 6222094
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROEMQVIST, Mats
APPLICANT: BERGSTROM, Sven
APPLICANT: HERNELL, Olle
APPLICANT: Toernell, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
TITLE OF INVENTION: OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 857 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 45..593
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 45..593
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 45..104
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 13..44
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 594...848
US-08-256-799-1

Alignment Scores:
Pred. No.: 11.7 Length: 857
Score: 63.00 Matches: 17
Percent Similarity: 50.85% Conservative: 13
Best Local Similarity: 28.81% Mismatches: 25
Query Match: 19.94% Indels: 4
DB: 3 Gaps: 3

US-10-079-754A-10 (1-58) x US-08-256-799-1 (1-857)

Qy	1	MetLysIlePheIlePheValPhe--IleMetAlaLeuIleLeuAlaMetIleArgAla	19
Db	45	ATGAGAGATTTCCTCTAGTTGTCAATGCCCTGCCATTAAACCTTCTTTTGGCTGTG	104
Qy	20	AspSerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGln	39
Db	105	GAGGTTCAAAACCAACCAACACAGCATGCCATGAGAATGATGAAGACCATCTATCAG	164
Qy	40	GlnTyrGlnProTyrGlnArgTyrProLeuasnTyr---ProProAlaTyrProPhe	57
Db	165	AAACAGCTCCATAT-----GTCCCAATGATTATGTGCCAAATAGCTATCCTTAT	215

Search completed: August 16, 2004, 00:49:11
Job time : 1484 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus_p2n model

Run on: August 16, 2004, 00:23:24 ; Search time 326 Seconds
(without alignments) 872.955 Million cell updates/sec

Title: US-10-079-754A-10

Perfect score: 316
Sequence: 1 MKIPIFVFNALILAMIRAD.....QQYQYQYPLNYPPAVPFP 58

Scoring table: BLOSUM62

Scoring scheme:

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Minimum	DB seq	length:
Maximum	DB seq	length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-QB/cgcn2_1/US10FO spec/U01097954/runat_06082004_181230_29453/app_query_fasta_1.199
-DB=Published Applications NA -OPMT=fastap -SUFFIX=snb -MINMATCH=0.1
-LOCPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRCONS=human40 cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODS=LOCAL -OUTEXT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-NAXLEN=200000000 -USER=US10379754_@CGN_1_480_@runat_06082004_181230_29453
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPEXT=0.5
-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -XDELET=7
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Database : Published Applications NA:**

Database	Published	Application	PK
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3:	/cgn2	6/pdata/2/pubpna/US06_NEW	PUB.seq.*
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5:	/cgn2	6/pdata/2/pubpna/US07_NEW	PUB.seq.*
6:	/cgn2	6/pdata/2/pubpna/PCTUS_NEW	PUBCOMB.seq.*
7:	/cgn2	6/pdata/2/pubpna/US08_NEW	PUB.seq.*
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9:	/cgn2	6/pdata/2/pubpna/US09A_PUBCOMB	.seq.*
10:	/cgn2	6/pdata/2/pubpna/US09B_PUBCOMB	.seq.*
11:	/cgn2	6/pdata/2/pubpna/US09C_PUBCOMB	.seq.*
12:	/cgn2	6/pdata/2/pubpna/US09_NEW	PUB.seq.*
13:	/cgn2	6/pdata/2/pubpna/US09_PUBCOMB	.seq.*
14:	/cgn2	6/pdata/2/pubpna/US10A_PUBCOMB	.seq.*
15:	/cgn2	6/pdata/2/pubpna/US10B_PUBCOMB	.seq.*
16:	/cgn2	6/pdata/2/pubpna/US10C_PUBCOMB	.seq.*
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19:	/cgn2	6/pdata/2/pubpna/US60_PUBCOMB	.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	100	100	100	100	100	100

ALIGNMENTS

RESULT 1

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US-00-079-754A-15
; Sequence 15, Application US/10079754A
; Publication No. US2002016425A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15

```

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 15

; LENGTH: 267

; TYPE: DNA

; ORGANISM: Bovine

US-10-079-754A-15

Alignment Scores:

Pred. No.: 7,07e-37 Length: 267
Score: 316.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-15 (1-267)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
|||||
DB 44 ATGAAGATCTTTATCTTTGCTTCTTATATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
|||||
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40
|||||
DB 104 TCATCTGAAGAGAAACGTCACAGGAAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
|||||
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
|||||
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217
|||||

RESULT 2

US-10-079-623-200

; Sequence 200, Application US/10079623

; Publication No. US20020169302A1

; GENERAL INFORMATION:

; APPLICANT: Havukkala, Ilkka J.

; APPLICANT: Glenn, Matthew

; APPLICANT: Grigor, Murray R.

; APPLICANT: Molenaar, Adrian J.

; TITLE OF INVENTION: Compositions isolated from bovine

; FILE OF INVENTION: mammary gland and methods for their use.

; FILE REFERENCE: 11000.1044C3

; CURRENT APPLICATION NUMBER: US/10/079,623

; NUMBER OF SEQ ID NOS: 370

; CURRENT FILING DATE: 2002-02-19

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 200

; LENGTH: 267

; TYPE: DNA

; ORGANISM: Bovine

US-10-079-623-200

Alignment Scores:

Pred. No.: 7,07e-37 Length: 267
Score: 316.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-623-200 (1-267)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
|||||
DB 44 ATGAAGATCTTTATCTTTGCTTCTTATATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
|||||
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40
|||||
DB 104 TCATCTGAAGAGAAACGTCACAGGAAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
|||||
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
|||||
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217
|||||

RESULT 3

US-10-079-754A-1

; Sequence 1, Application US/10079754A

; Publication No. US20020164625A1

; GENERAL INFORMATION:

; APPLICANT: Glenn, Matthew

; APPLICANT: Grigor, Murray R.

; APPLICANT: Molenaar, Adrian J.

; APPLICANT: Davis, Stephen R.

; TITLE OF INVENTION: Compositions Isolated from Bovine

; FILE OF INVENTION: Mammary Gland and Methods for Their Use

; FILE REFERENCE: 11000.1068

; CURRENT APPLICATION NUMBER: US/10/079,754A

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: US 09/699,146

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60,162,701

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: US 09/644,190

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: US 60,150,330

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 505

; TYPE: DNA

; ORGANISM: Bovine

US-10-079-754A-1

Alignment Scores:

Pred. No.: 1,68e-36 Length: 505
Score: 316.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-1 (1-505)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
|||||
DB 44 ATGAAGATCTTTATCTTTGCTTCTTATATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
|||||
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40
|||||
DB 104 TCATCTGAAGAGAAACGTCACAGGAAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
|||||
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
|||||
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217
|||||

RESULT 4

US-10-079-754A-4

; Sequence 4, Application US/10079754A

; Publication No. US20020164625A1

; GENERAL INFORMATION:

; APPLICANT: Glenn, Matthew

; APPLICANT: Grigor, Murray R.

; APPLICANT: Molenaar, Adrian J.

; APPLICANT: Davis, Stephen R.

; TITLE OF INVENTION: Compositions Isolated from Bovine

; FILE OF INVENTION: Mammary Gland and Methods for Their Use

; FILE REFERENCE: 11000.1068

; CURRENT APPLICATION NUMBER: US/10/079,754A

; CURRENT FILING DATE: 2002-02-19

; PRIOR APPLICATION NUMBER: US 09/699,146

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60,162,701

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: US 09/644,190

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: US 60,150,330

```

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-4

```

```

Alignment Scores:
Pred. No.: 2,15e-36 Length: 604
Score: 316.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

```

US-10-079-754A-10 (1-58) x US-10-079-754A-4 (1-604)

```

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaasp 20
Db 154 ATGAAGATCTTTATCTTTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 213
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40
Db 214 TCATCTGAAGAGAAACGTCACAGAAACGGAACAAACATCATAGAGATATTTTCAACAA 273
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
Db 274 TACCAGCCATATCAACGATATCCACTAAATATCTCTCGTATCCATTTCCT 327

```

RESULT 5

```

US-10-079-754A-2
; Sequence 2, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-2

```

```

Alignment Scores:
Pred. No.: 2,88e-36 Length: 585
Score: 315.00 Matches: 57
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.28% Mismatches: 0
Query Match: 99.68% Indels: 0
DB: 14 Gaps: 0

```

US-10-079-754A-10 (1-58) x US-10-079-754A-2 (1-585)

```

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaasp 20

```

```

Db 149 ATGAAGATCTTTATCTTTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 208
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40
Db 209 TCATCTGAAGAGAAACGTCACAGAAACGGAACAAACATCATAGAGATATTTTCAACAA 268
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58
Db 269 TACCAGCCATATCAACGATATCCACTAAATATCTCTCGTATCCATTTCCT 322

```

RESULT 6

```

US-10-079-754A-6
; Sequence 6, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-6

```

Alignment Scores:

```

Pred. No.: 8,66e-31 Length: 525
Score: 277.00 Matches: 57
Percent Similarity: 82.61% Conservative: 0
Best Local Similarity: 82.61% Mismatches: 12
Query Match: 87.66% Indels: 1
DB: 14 Gaps: 1

```

US-10-079-754A-10 (1-58) x US-10-079-754A-6 (1-525)

```

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaasp 20
Db 43 ATGAAGATCTTTATCTTTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 102
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArg----- 35
Db 103 TCATCTGAAGAGAAACGTCACAGAAACGGAACAAACATCATGT-TGATAGTCTCCAGA 161
QY 36 -----GlyTyrPheGlnGlnTyrGlnProTyrGlnArgTyrProleu 49
Db 162 ATTCTTTACTAATAACAGAGGATATTTTCAACAATACCAACCATATCAGCATATCCACTA 221

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QY 50 AsnTyrProProAlaTyrProPhePro 58
Db 222 AATTATCTCTCTCGTATCCATTTCCT 248

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RESULT 7

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US-10-079-754A-3
; Sequence 3, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.

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1097 ATGAAGTTCCCTTGTCTTTGGCCTTCACTTTGGCTCTCATGGTTTCCATGATTGGAGCTGAT 1156

; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-23
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA_signal
; LOCATION: 397..402
; NAME/KEY: polyA_site
; LOCATION: 423..438
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 397..402
; NAME/KEY: polyA_site
; LOCATION: 423..438
US-09-999-570-5

Alignment Scores:

Pred. No.:	0.000281	Length:	438
Score:	94.50	Matches:	18
Percent Similarity:	56.36%	Conservative:	13
Best Local Similarity:	32.73%	Mismatches:	17
Query Match:	29.91%	Indels:	7
DB:	10	Gaps:	1

US-10-079-754A-10 (1-58) x US-09-999-570-5 (1-438)

QY	1	MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaASP	20
Db	84	ATGAAGTTTTTTTGCTTTGCTTTAGTCTTGGCTCTCATGATTTCCATGATTAGCGCTGAT	143
QY	21	SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln	40
Db	144	TCACATGAAGAAGACATCATGGGTATAGAGAAAATTCAT	185
QY	41	TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr	55
Db	186	---GAAAAGCATCATTCATACCATATCACACTACTACCATCTTTT	227

RESULT 15

US-10-000-489-5
; Sequence 5, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
; APPLICANT: BenJanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91 US6 DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA_signal
; LOCATION: 397..402
; NAME/KEY: polyA_site
; LOCATION: 423..438
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 397..402
; NAME/KEY: polyA_site
; LOCATION: 423..438
US-10-000-489-5

Alignment Scores:

Pred. No.:	0.000281	Length:	438
Score:	94.50	Matches:	18
Percent Similarity:	56.36%	Conservative:	13
Best Local Similarity:	32.73%	Mismatches:	17
Query Match:	29.91%	Indels:	7
DB:	15	Gaps:	1

US-10-079-754A-10 (1-58) x US-10-000-489-5 (1-438)

QY	1	MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaasp	20
Db	84	ATGAAGTTTTTTTGCTTTGCTTTAGTCTTGGCTCTCATGATTTCCATGATTAGCGCTGAT	143
QY	21	SerSerGluGluLysArgHisArgLysArgLysHisHisArgGlyTyrPheGlnGln	40
Db	144	TCACATGAAGAAGACATCATGGGTATAGAGAAAATTCAT	185
QY	41	TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyr	55
Db	186	---GAAAAGCATCATTCATACCATATCACACTACTACCATCTTTT	227

Search completed: August 16, 2004, 01:12:54
Job time : 331 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 6, 2004, 17:06:10 ; Search time 18 Seconds
(without alignments)
166.350 Million cell updates/sec

Title: US-10-079-754A-10

Perfect score: 58

Sequence: 1 MKIFIFVFMALILMIRAD.....QQYQYQRYPLNYPYPPFP 58

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B.COMB.pap.*
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4: /cgn2_6/ptodata/2/iaa/6B.COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	10.3	12	3	US-08-602-999A-268
2	6	10.3	12	4	US-09-500-124-268
3	6	10.3	95	4	US-09-621-976-7261
4	6	10.3	103	4	US-09-460-384-35
5	6	10.3	107	4	US-09-198-452A-1200
6	6	10.3	134	4	US-09-634-238-376
7	6	10.3	146	4	US-09-489-039A-7386
8	6	10.3	164	4	US-09-134-000C-3551
9	6	10.3	201	4	US-09-543-681A-4214
10	6	10.3	216	4	US-09-543-681A-5885
11	6	10.3	241	4	US-09-489-039A-8060
12	6	10.3	263	4	US-09-134-001C-3062
13	6	10.3	298	4	US-09-543-681A-5642
14	6	10.3	310	3	US-08-605-284B-16
15	6	10.3	380	3	US-09-097-889-25
16	6	10.3	380	4	US-09-098-079-25
17	6	10.3	386	4	US-09-489-039A-8756
18	6	10.3	450	4	US-09-369-247-97
19	6	10.3	508	4	US-09-369-247-167
20	6	10.3	511	4	US-09-543-681A-6490
21	6	10.3	511	4	US-09-134-000C-5362
22	6	10.3	539	4	US-09-291-922-26
23	6	10.3	581	4	US-09-489-039A-10559
24	6	10.3	590	4	US-09-134-001C-4390
25	6	10.3	601	4	US-09-336-643A-4
26	6	10.3	623	4	US-09-540-236-1934
27	6	10.3	751	4	US-09-252-991A-29893

28	6	10.3	1026	1	US-07-998-003A-95	Sequence 95, Appl
29	6	10.3	1026	1	US-08-453-274B-95	Sequence 95, Appl
30	6	10.3	1026	1	US-08-453-695A-95	Sequence 95, Appl
31	6	10.3	1026	1	US-08-268-161A-95	Sequence 95, Appl
32	6	10.3	1026	2	US-08-453-702A-95	Sequence 95, Appl
33	6	10.3	1026	3	US-09-099-639-95	Sequence 95, Appl
34	6	10.3	1026	5	PCT-US93-12588-95	Sequence 95, Appl
35	6	10.3	1026	5	PCT-US95-08071-95	Sequence 95, Appl
36	6	10.3	1203	1	US-07-998-003A-103	Sequence 103, App
37	6	10.3	1203	1	US-08-453-274B-103	Sequence 103, App
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40	6	10.3	1203	2	US-08-453-702A-103	Sequence 103, App
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42	6	10.3	1203	5	PCT-US93-12588-103	Sequence 103, App
43	6	10.3	1203	5	PCT-US95-08071-103	Sequence 103, App
44	6	10.3	1349	3	US-08-938-291A-6	Sequence 6, Appl
45	6	10.3	1349	4	US-09-589-619-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-602-999A-268
; Sequence 268, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 750-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-268

Query Match 10.3%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 YPPAYP 56
|||||
Db 1 YPPAYP 6

RESULT 2
US-09-500-124-268
; Sequence 268, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-268

Query Match 10.3%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 YPPAYP 56
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Db 1 YPPAYP 6

RESULT 3
US-09-621-976-7261
; Sequence 7261, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7261
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7261

Query Match 10.3%; Score 6; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SEEKRH 27
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Db 86 SEEKRH 91

RESULT 4

US-09-460-384-35
; Sequence 35, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
; APPLICANT: EL TAYAR, Nabil
; BLECHNER, Steven
; JAMESON, Brad
; TEPPER, Mark
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
; PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
; SAME
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,384
; FILING DATE: 13-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/12312
; FILING DATE: 11-JUN-1998
; APPLICATION NUMBER: US 60/049,470
; FILING DATE: 12-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: EL TAYAR=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-460-384-35

Query Match 10.3%; Score 6; DB 4; Length 103;

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Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 QQYQPY 44
Db 88 QQYQPY 93

RESULT 5
US-09-198-452A-1200
; Sequence 1200, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1200
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1200

Query Match 10.3%; Score 6; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SSEEKR 26
Db 80 SSEEKR 85

RESULT 6
US-09-634-238-376
; Sequence 376, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Iikka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043UI
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-376

Query Match 10.3%; Score 6; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 YPPAYP 56
Db 52 YPPAYP 57

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RESULT 7
US-09-489-039A-7386
; Sequence 7386, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7386
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7386

Query Match 10.3%; Score 6; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 RADSSSE 23
Db 90 RADSSSE 95

RESULT 8
US-09-134-000C-3551
; Sequence 3551, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3551
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3551

Query Match 10.3%; Score 6; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SSEEKR 26
Db 151 SSEEKR 156

RESULT 9
US-09-543-681A-4214
; Sequence 4214, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

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; SEQ ID NO 4214
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4214

Query Match      10.3%; Score 6; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 MALILA 15
Db      105 MALILA 110
|||||

RESULT 10
US-09-543-681A-5885
; Sequence 5885, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5885
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5885

Query Match      10.3%; Score 6; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FIMALI 13
Db      28 FIMALI 33
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RESULT 11
US-09-489-039A-8060
; Sequence 8060, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8060
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8060

Query Match      10.3%; Score 6; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FIMALI 13
Db      183 FIMALI 188
|||||

; SEQ ID NO 4214
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4214

Query Match      10.3%; Score 6; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 MALILA 15
Db      105 MALILA 110
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RESULT 12
US-09-134-001C-3062
; Sequence 3062, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GIC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3062
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3062

Query Match      10.3%; Score 6; DB 4; Length 263;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FIFVEI 9
Db      10 FIFVEI 15
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RESULT 13
US-09-543-681A-5642
; Sequence 5642, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5642
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5642

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Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 SSEEKR 26
Db      264 SSEEKR 269
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RESULT 14
US-08-605-284B-16
; Sequence 16, Application US/08605284B
; Patent No. 6060271
; GENERAL INFORMATION:
; APPLICANT: WALEWSKI, JOSE L.
; APPLICANT: RECIO-PINTO, ESPERANZA
; TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
; TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
; STREET: CLINTON SQUARE, P.O. BOX 1051
```



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; CITY: ROCHESTER
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,284B
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BRAMAN, SUSAN J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-605-284B-16

Query Match      10.3%; Score 6; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 FINALI 13
      |||||
Db      67 FINALI 72

RESULT 15
US-09-097-889-25
; Sequence 25, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Heintzstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,889
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-097-889-25

Query Match      10.3%; Score 6; DB 3; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      299 LILAMI 304

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-10-079-754A-10

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SUMMARIES

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5	27	46.6	70	13	US-10-079-754A-9
6	11	19.0	21	13	US-10-079-754A-11
7	8	13.8	363	12	US-10-425-114-70822
8	7	12.1	13	10	US-09-876-904A-586
9	7	12.1	62	12	US-10-210-172-168
10	7	12.1	72	12	US-10-424-599-145633
11	7	12.1	150	12	US-10-424-599-257786
12	6	10.3	12	9	US-09-927-436-1
13	6	10.3	12	14	US-10-161-791-268
14	6	10.3	47	12	US-10-210-172-170
15	6	10.3	52	12	US-10-424-599-164611

16 6 10.3 56 11 US-09-864-408A-774 Sequence 774, App
17 6 10.3 62 12 US-10-424-599-229298 Sequence 229298,
18 6 10.3 63 14 US-10-125-258-56 Sequence 56, Appl
19 6 10.3 63 14 US-10-125-258-61 Sequence 61, Appl
20 6 10.3 71 12 US-10-424-599-156798 Sequence 156798,
21 6 10.3 71 12 US-10-424-599-221250 Sequence 221250,
22 6 10.3 71 12 US-10-424-599-250830 Sequence 250830,
23 6 10.3 72 16 US-10-437-963-178932 Sequence 178932,
24 6 10.3 75 9 US-09-864-761-47763 Sequence 47763, A
25 6 10.3 81 12 US-10-424-599-225829 Sequence 225829,
26 6 10.3 96 12 US-10-424-599-169059 Sequence 169059,
27 6 10.3 99 12 US-10-424-599-266340 Sequence 266340,
28 6 10.3 106 11 US-09-833-445-791 Sequence 791, App
29 6 10.3 107 12 US-10-424-599-224333 Sequence 224333,
30 6 10.3 107 15 US-10-289-762-1200 Sequence 1200, Ap
31 6 10.3 108 9 US-09-738-626-6237 Sequence 6237, Ap
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35 6 10.3 117 12 US-10-424-599-216096 Sequence 216096,
36 6 10.3 119 12 US-10-424-599-145916 Sequence 145916,
37 6 10.3 125 16 US-10-437-963-158794 Sequence 158794,
38 6 10.3 126 12 US-10-282-122A-73863 Sequence 73863, A
39 6 10.3 130 13 US-10-001-857-205 Sequence 205, App
40 6 10.3 144 12 US-10-424-599-159623 Sequence 159623,
41 6 10.3 153 12 US-10-424-599-159363 Sequence 159363,
42 6 10.3 161 12 US-10-424-599-203488 Sequence 203488,
43 6 10.3 161 12 US-10-424-599-279792 Sequence 279792,
44 6 10.3 161 16 US-10-408-765A-2076 Sequence 2076, Ap
45 6 10.3 161 16 US-10-437-963-200341 Sequence 200341,

ALIGNMENTS

RESULT 1

US-10-079-754A-7
; Sequence 7, Application US/10079754A
; Publication No. US2002016425A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 1100C.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-7

Query Match 100.0%; Score 58; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.9e-53;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKIFIFVFMALILAMIRADSEEEKHRRKXKHRRGYFQQYQYQRYPLNPPAYPPF 58
Db 1 MKIFIFVFMALILAMIRADSEEEKHRRKXKHRRGYFQQYQYQRYPLNPPAYPPF 58

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US-10-079-754A-10
; Sequence 10, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-10

Query Match 100.0%; Score 58; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 6.9e-53; Indels 0; Gaps 0;
Matches 58; Conservative 0; Mismatches 0;

QY 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHHRGYFQQYQYQRYPLNYPAYPPP 58
DB 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHHRGYFQQYQYQRYPLNYPAYPPP 58

RESULT 3
US-10-079-754A-8
; Sequence 8, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-8

Query Match 87.9%; Score 51; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-45; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 0;

US-10-079-754A-12
; Sequence 12, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-12

Query Match 58.6%; Score 34; DB 13; Length 59;
Best Local Similarity 100.0%; Pred. No. 7.2e-28; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHH 34
DB 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHH 34

RESULT 5
US-10-079-754A-9
; Sequence 9, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-9

Query Match 100.0%; Score 51; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-45; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 0;

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Query Match 10.3%; Score 6; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 KRKKGH 34
DB 3 KRKKGH 8

RESULT 13

US-10-161-791-268
; Sequence 268, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana W.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 268:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-268

Query Match 10.3%; Score 6; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 YPPAYP 56
DB 1 YPPAYP 6

RESULT 14

US-10-210-172-170
; Sequence 170, Application US/10210172
; Publication No. US20040043928A1

GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalt, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-01
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 170
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-170

Query Match 10.3%; Score 6; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DSSEK 25
DB 3 DSSEK 8

```
RESULT 15
US-10-424-599-164611
; Sequence 164611, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164611
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(52)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_119661C.1.pep
US-10-424-599-164611

Query Match      10.3%; Score 6; DB 12; Length 52;
Best Local Similarity 100.0%; Pred.No. 97;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 PYQRYP 48
DB      35 PYQRYP 40
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Search completed: August 6, 2004, 17:15:03
Job time : 47 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	63	19.9	182	1	US-07-962-569A-8	Sequence 8, Appli
2	63	19.9	182	1	US-08-308-883-2	Sequence 2, Appli
3	63	19.9	182	1	US-08-730-163-2	Sequence 2, Appli
4	63	19.9	182	3	US-08-256-799-2	Sequence 2, Appli
5	63	19.9	182	3	US-08-462-437-2	Sequence 2, Appli
6	63	19.9	182	3	US-08-462-437-31	Sequence 31, Appli
7	62	19.6	248	4	US-09-252-991A-27856	Sequence 27856, A
8	61.5	19.5	729	4	US-09-525-188-20	Sequence 20, Appli
9	61	19.3	620	4	US-09-525-188-20	Sequence 20, Appli
10	59.5	18.8	271	4	US-09-134-000C-4463	Sequence 4463, Ap
11	59	18.7	225	4	US-09-252-991A-16848	Sequence 16848, A
12	59	18.7	225	4	US-09-252-991A-27348	Sequence 27348, A
13	58.5	18.5	247	4	US-09-252-991A-21881	Sequence 21881, A
14	58.5	18.5	333	4	US-09-252-991A-27419	Sequence 27419, A
15	58	18.4	521	4	US-09-252-991A-20994	Sequence 20994, A
16	58	18.4	585	4	US-09-196-270-4	Sequence 30311, A
17	57.5	18.2	404	3	US-09-046-578-2	Sequence 4, Appli
18	56.5	17.9	997	4	US-09-252-991A-30799	Sequence 30799, A
19	56.5	17.9	1290	3	US-09-250-460B-6	Sequence 6, Appli
20	56.5	17.9	1619	4	US-09-392-812A-4	Sequence 4, Appli
21	56	17.7	137	4	US-09-247-155-109	Sequence 109, App
22	56	17.7	155	4	US-09-148-545-164	Sequence 164, App
23	56	17.7	155	4	US-09-148-545-225	Sequence 225, App
24	56	17.7	172	4	US-09-148-039A-12246	Sequence 12246, A
25	56	17.7	279	4	US-09-489-039A-32443	Sequence 32443, A
26	56	17.7	281	2	US-08-282-991A-35443	Sequence 6, Appli
27	56	17.7	413	4	US-09-489-039A-9137	Sequence 9137, Ap

CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHOR: L. Hansson et al
TITLE: DNA Encoding kappa-Casein, Process for Obtaining the Protein and Use Thereof
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER: PCT/WO93/15196
FILING DATE: 25-JAN-1993
PUBLICATION DATE: 05-AUG-1993
RELEVANT RESIDUES IN SEQ ID NO:
US-08-730-163-2
Query Match 19.9%; Score 63; DB 1; Length 182;
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels 4; Gaps 3;
QY 1 MKIFIFVF-IMALLIAMIRADSSSEKRRKXKXHHRGYFQQYQYQRYPLNY-PPAYPF 57
Db 1 MKSFLVNVNALLTLPLAVEVQKQKQACHENDERPFYQKTAPY--VPMYYVNSVPY 57
RESULT 4
US-08-256-799-2
Sequence 2, Application US/08256799
Patent No. 6222094
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROEMQVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELL, Olle
APPLICANT: Toernell, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS FOR
OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,799
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-256-799-2
Query Match 19.9%; Score 63; DB 3; Length 182;
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels 4; Gaps 3;
QY 1 MKIFIFVF-IMALLIAMIRADSSSEKRRKXKXHHRGYFQQYQYQRYPLNY-PPAYPF 57
Db 1 MKSFLVNVNALLTLPLAVEVQKQKQACHENDERPFYQKTAPY--VPMYYVNSVPY 57
RESULT 5
US-08-462-437-2
Sequence 2, Application US/08462437
Patent No. 6232094
GENERAL INFORMATION:
APPLICANT: HANSSON, Lennart
APPLICANT: STROEMQVIST, Mats
APPLICANT: BERGSTROEM, Sven
APPLICANT: HERNELL, Olle
APPLICANT: Toernell, Jan
TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
OBTAINING THE PROTEIN AND USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,437
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 88/92
FILING DATE: 23-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: HANSSON=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-437-2
Query Match 19.9%; Score 63; DB 3; Length 182;
Best Local Similarity 28.8%; Pred. No. 2.3;
Matches 17; Conservative 13; Mismatches 25; Indels 4; Gaps 3;
QY 1 MKIFIFVF-IMALLIAMIRADSSSEKRRKXKXHHRGYFQQYQYQRYPLNY-PPAYPF 57

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DB      1  MKSFLVVNALTLPLAVEVQKQKACHENDERPFYQKTAPY--VPMYIVVNSIPY 5
RESULT 6
US-08-462-437-31
; Sequence 31, Application US/08462437
; Patent No. 6232094
; GENERAL INFORMATION:
; APPLICANT: HANSSON, Lennart
; APPLICANT: STROEMQVIST, Mats
; APPLICANT: BERGSTROEM, Sven
; APPLICANT: HERNELL, Oile
; APPLICANT: TOERNELL, Jan
; TITLE OF INVENTION: DNA ENCODING KAPPA-CASEIN, PROCESS
; TITLE OF INVENTION: FOR OBTAINING THE PROTEIN AND USE THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,437
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 88/92
; FILING DATE: 23-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: HANSSON=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-437-31
Best Match 19.9%; Score 63; DB 3; Length 182;
Best Local Similarity 28.8%; Pred.No.2.3;
Matches 17; Conservative 13; Mismatches 25; Indels 4; Gaps

QY      1  MKKIFIFVF-IMALLIMIRADSSSEKRRKKHGGYEQQYQYQYPLANY-PPAYEYF 57
|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB      1  MKSFLVVNALTLPLAVEVQKQKACHENDERPFYQKTAPY--VPMYIVVNSIPY 57
RESULT 7
US-09-252-991A-27856
; Sequence 27856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
US-09-252-991A-27856
; Sequence 27856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21881
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21881

Query Match      18.7%; Score 59; DB 4; Length 720;
Best Local Similarity 29.8%; Pred. No. 32;
Matches 14; Conservative 8; Mismatches 15; Indels 10; Gaps 1;

QY      18 RADSSSEKHKRKKKH-----RCYFOQYQPYQRYPLNPPA 54
      ||:||||:||||
Db      325 RAGQPPRRHQRRHHPGGRPAGORPAGTGORQGPARRQPRPAPA 371

RESULT 13
US-09-252-991A-27419
; Sequence 27419, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27419
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27419

Query Match      18.5%; Score 58.5; DB 4; Length 247;
Best Local Similarity 39.4%; Pred. No. 11;
Matches 13; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

QY      18 RADSSSEKHKRKKKHGCVFOQYQRYPLN 50
Db      60 RRDTGGRHPRRLDHRHRRQQQPP---HPLN 89

RESULT 14
US-09-252-991A-20994
; Sequence 20994, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20994
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20994

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Query Match      18.5%; Score 58.5; DB 4; Length 333;
Best Local Similarity 38.7%; Pred. No. 16;
Matches 12; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

QY      25 KRHRKRK---KHHRGYFQQYQYQYQYPLNYP 52
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Db      114 RHHHRPDQGTTHRGRLRQGLPVRRLPADHP 144

RESULT 15
US-09-252-991A-30311
; Sequence 30311, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30311
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30311

Query Match      18.4%; Score 58; DB 4; Length 521;
Best Local Similarity 36.7%; Pred. No. 30;
Matches 18; Conservative 6; Mismatches 21; Indels 4; Gaps 2;

QY      12 LILAMIRADSSE--EKHRKRKHHRGYFQQYQYQYQYPLNYPYPFP 58
      ||| | | | | | | | | | | | | | | |
Db      45 LIRRTIAAGGVEIVEHRRHRRHLLHQLRQRQLRQ--RHRFAHQRP 91
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Search completed: August 6, 2004, 17:05:15
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 6, 2004, 17:04:44 ; Search time 47 seconds
(without alignments)

387.098 Million cell updates/sec

Title: US-10-079-754A-10

Perfect score: 316
Sequence: 1 MKIFIFVFMALILAMIRAD.....QQYQYQRYPLNYPPAYPFP 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	316	100.0	58	US-10-079-754A-7	Sequence 7, Appli
2	316	100.0	58	US-10-079-754A-10	Sequence 10, Appli
3	315	99.7	58	US-10-079-754A-8	Sequence 8, Appli
4	170	53.8	59	US-10-079-754A-12	Sequence 12, Appli
5	169	53.5	70	US-10-079-754A-9	Sequence 9, Appli
6	112	35.4	21	US-10-079-754A-11	Sequence 11, Appli
7	110	34.8	62	US-10-210-172-168	Sequence 168, App
8	95	30.1	51	US-09-917-340-19	Sequence 19, Appli
9	94.5	29.9	78	US-09-992-600A-6	Sequence 6, Appli
10	94.5	29.9	78	US-09-924-340-6	Sequence 6, Appli
11	94.5	29.9	78	US-09-992-095B-6	Sequence 6, Appli
12	94.5	29.9	78	US-09-999-570-6	Sequence 6, Appli
13	94.5	29.9	78	US-10-000-489-6	Sequence 6, Appli
14	94.5	29.9	78	US-10-000-986-6	Sequence 6, Appli
15	94.5	29.9	78	US-10-154-678-6	Sequence 6, Appli

16	22.8	1504	16	US-10-437-963-192104	Sequence 192104,
17	22.8	1680	16	US-10-437-963-192175	Sequence 192175,
18	22.2	1363	16	US-10-437-963-192041	Sequence 192041,
19	21.8	229	12	US-10-282-122A-71761	Sequence 71761, A
20	21.5	1822	16	US-10-437-963-192099	Sequence 192099,
21	20.9	277	16	US-10-631-581-22	Sequence 22, Appli
22	20.6	1081	16	US-10-437-963-191989	Sequence 191989,
23	20.6	1199	16	US-10-437-963-192108	Sequence 192108,
24	20.6	1403	16	US-10-437-963-191987	Sequence 191987,
25	20.6	1487	16	US-10-437-963-188109	Sequence 188109,
26	20.6	1504	15	US-10-374-780A-1457	Sequence 1457, Ap
27	20.6	1504	16	US-10-437-963-192134	Sequence 192134,
28	20.6	1516	16	US-10-437-963-192071	Sequence 192071,
29	20.6	1542	16	US-10-437-963-192098	Sequence 192098,
30	20.6	1562	15	US-10-374-780A-1458	Sequence 1458, Ap
31	20.6	1562	15	US-10-374-780A-1459	Sequence 1459, Ap
32	20.6	1571	16	US-10-437-963-192152	Sequence 192152,
33	20.6	1572	16	US-10-437-963-192213	Sequence 192213,
34	20.6	1595	16	US-10-437-963-179538	Sequence 179538,
35	20.6	1629	16	US-10-437-963-192058	Sequence 192058,
36	20.6	1681	16	US-10-437-963-191994	Sequence 191994,
37	20.6	1694	16	US-10-437-963-192057	Sequence 192057,
38	20.6	1732	16	US-10-437-963-192167	Sequence 192167,
39	20.6	1761	16	US-10-437-963-192096	Sequence 192096,
40	20.6	1764	16	US-10-437-963-192101	Sequence 192101,
41	20.6	1776	16	US-10-437-963-179541	Sequence 179541,
42	20.6	1792	16	US-10-437-963-192174	Sequence 192174,
43	20.6	1809	16	US-10-437-963-192109	Sequence 192109,
44	20.6	1815	16	US-10-437-963-192168	Sequence 192168,
45	20.6	1820	16	US-10-437-963-192165	Sequence 192165,

ALIGNMENTS

RESULT 1

US-10-079-754A-7
; Sequence 7, Application US/10079754A
; Publication No. US2002016425A1
; GENERAL INFORMATION:
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-7

Query Match 100.0%; Score 316; DB 13; Length 58;

Best Local Similarity 100.0%; Pred. No. 5.6e-30; Indels 0; Gaps 0;
Matches 58; Conservative 0; Mismatches 0;

QY 1 MKIFIFVFMALILAMIRADSEKRRKXKHHRGYFQQYQYQRYPLNYPPAYPFP 58

Db 1 MKIFIFVFMALILAMIRADSEKRRKXKHHRGYFQQYQYQRYPLNYPPAYPFP 58

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RESULT 2
US-10-079-754A-10
; Sequence 10, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-10

Query Match 100.0%; Score 316; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 5.6e-30;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKKHGRGYFQQYQYQRYPLNYPAYPPF 58
DB 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKKHGRGYFQQYQYQRYPLNYPAYPPF 58

RESULT 3
US-10-079-754A-8
; Sequence 8, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-8

Query Match 99.7%; Score 315; DB 13; Length 58;
Best Local Similarity 98.3%; Pred. No. 7.4e-30;
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKKHGRGYFQQYQYQRYPLNYPAYPPF 58

RESULT 4
US-10-079-754A-12
; Sequence 12, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-12

Query Match 53.8%; Score 170; DB 13; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKKH 34

RESULT 5
US-10-079-754A-9
; Sequence 9, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-9

Query Match 99.7%; Score 315; DB 13; Length 58;
Best Local Similarity 98.3%; Pred. No. 7.4e-30;
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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US-10-079-754A-9
Query Match      53.5%; Score 169; DB 13; Length 70;
Best Local Similarity 97.1%; Pred. No. 1.7e-12;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHH 34

RESULT 6
US-10-079-754A-11
; Sequence 11, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.11068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-11

Query Match      35.4%; Score 112; DB 13; Length 21;
Best Local Similarity 94.7%; Pred. No. 2.5e-06;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FQQQYQYQRYPLNYPYPAYP 19

RESULT 7
US-10-210-172-168
; Sequence 168, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Rekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Murallidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia

US-10-079-754A-10
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Ford
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
; APPLICANT: Edinger, Shlomit
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-416 A
; CURRENT APPLICATION NUMBER: US/10/210,172
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 168
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-210-172-168

Query Match      34.8%; Score 110; DB 12; Length 62;
Best Local Similarity 49.1%; Pred. No. 1.4e-05;
Matches 27; Conservative 7; Mismatches 19; Indels 2; Gaps 2;

Qy 1 MKIFIFVFMALILAMIRADSSSEKRRKRRKHHGYYFOQYQYQRYPLNYPAY 55
Db 1 MKFLVFAFILALMVSMIGADSSSEKFLRRIGRFGYGY-CPYQVPPEQL-YQPY 53

RESULT 8
US-09-917-340-19
; Sequence 19, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McNulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 19

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-917-340-19

Query Match 30.1%; Score 95; DB 9; Length 51;

Best Local Similarity 46.8%; Pred. No. 0.00067;

Matches 22; Conservative 6; Mismatches 13; Indels 7; Gaps 2;

QY 1 MKIFIFVFMALILAMIRADSSSEKHKH-RKKKH-----HRGYFQQY 41

DB 1 MKFFVFALVLTALMISMTSADSHKRRHGHGKRRKFKHSHRGRYSNY 47

RESULT 9

US-09-992-600A-6

; Sequence 6, Application US/09992600A

; Publication No. US20030027161A1

; GENERAL INFORMATION:

; APPLICANT: Benjamin, Stephane

; APPLICANT: Tanaka, Hiroaki

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

; FILE REFERENCE: 91.US4.DIV

; CURRENT APPLICATION NUMBER: US/09/992,600A

; CURRENT FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 09/924,340

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: PCT/IB01/01715

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: JPatent

; SEQ ID NO 6

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: 1..19

US-09-992-600A-6

Query Match 29.9%; Score 94.5; DB 10; Length 78;

Best Local Similarity 32.7%; Pred. No. 0.0012;

Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 MKIFIFVFMALILAMIRADSSSEKHKHKKKHHRGYFQQYQYQYPLNYPAY 55

DB 1 MKFFVFALVLTALMISMTSADSHKRRHGHGKRRKFKH-----EKHSHYHTLLPLF 48

RESULT 10

US-09-924-340-6

; Sequence 6, Application US/09924340

; Publication No. US20030027248A1

; GENERAL INFORMATION:

; APPLICANT: Benjamin, Stephane

; APPLICANT: Tanaka, Hiroaki

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

; FILE REFERENCE: 91.US2.REG

; CURRENT APPLICATION NUMBER: US/09/924,340

; CURRENT FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: JPatent

; SEQ ID NO 6

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: 1..19

US-09-924-340-6

Query Match 29.9%; Score 94.5; DB 10; Length 78;

Best Local Similarity 32.7%; Pred. No. 0.0012;

Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 MKIFIFVFMALILAMIRADSSSEKHKHKKKHHRGYFQQYQYQYPLNYPAY 55

DB 1 MKFFVFALVLTALMISMTSADSHKRRHGHGKRRKFKH-----EKHSHYHTLLPLF 48

RESULT 11

US-09-992-095B-6

; Sequence 6, Application US/09992095B

; Publication No. US20030157485A1

; GENERAL INFORMATION:

; APPLICANT: Benjamin, Stephane

; APPLICANT: Tanaka, Hiroaki

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

; FILE REFERENCE: 91.US5.DIV

; CURRENT APPLICATION NUMBER: US/09/992,095B

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 09/924,340

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: PCT/IB01/01715

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: JPatent

; SEQ ID NO 6

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: 1..19

US-09-992-095B-6

Query Match 29.9%; Score 94.5; DB 10; Length 78;

Best Local Similarity 32.7%; Pred. No. 0.0012;

Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 MKIFIFVFMALILAMIRADSSSEKHKHKKKHHRGYFQQYQYQYPLNYPAY 55

DB 1 MKFFVFALVLTALMISMTSADSHKRRHGHGKRRKFKH-----EKHSHYHTLLPLF 48

RESULT 12

US-09-999-570-6

; Sequence 6, Application US/09999570

; Publication No. US20030170628A1

; GENERAL INFORMATION:

APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US08DIV
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-09-999-570-6

Query Match 29.9%; Score 94.5; DB 10; Length 78;
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 MKFIFVFMALILAMIRADSSSEKRRKRRKHHRGYFQQYQYQYPLNPPAY 55
DB 1 MKFFVFLVLMISMISADSHKRRHGYRRKFH-----EKHSHYHTLLPLF 48

RESULT 13

US-10-000-489-6
Sequence 6, Application US/10000489
Publication No. US2003009201A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-10-000-489-6

Query Match 29.9%; Score 94.5; DB 14; Length 78;

Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;
QY 1 MKFIFVFMALILAMIRADSSSEKRRKRRKHHRGYFQQYQYQYPLNPPAY 55
DB 1 MKFFVFLVLMISMISADSHKRRHGYRRKFH-----EKHSHYHTLLPLF 48

RESULT 14

US-10-000-986-6
Sequence 6, Application US/10000986
Publication No. US20030096247A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US9.DIV
CURRENT APPLICATION NUMBER: US/10/000,986
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
SEQ ID NO 6
LENGTH: 78
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..19
US-10-000-986-6

Query Match 29.9%; Score 94.5; DB 14; Length 78;
Best Local Similarity 32.7%; Pred. No. 0.0012;
Matches 18; Conservative 13; Mismatches 17; Indels 7; Gaps 1;

QY 1 MKFIFVFMALILAMIRADSSSEKRRKRRKHHRGYFQQYQYQYPLNPPAY 55
DB 1 MKFFVFLVLMISMISADSHKRRHGYRRKFH-----EKHSHYHTLLPLF 48

RESULT 15

US-10-154-678-6
Sequence 6, Application US/10154678
Publication No. US20030162186A1
GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182.US1.REG
CURRENT APPLICATION NUMBER: US/10/154,678
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 16, 2004, 00:50:06 ; Search time 61 Seconds
(without alignments)
527.658 Million cell updates/sec

Title: US-10-079-754A-10

Perfect score: 58

Sequence: 1 MKTIFVFMALILAMTRAD.....QQYQYQYPLNPPAYPPF 58

Scoring table:

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 652709 seqs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360396

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Issued.Patents NA -QMT=fastp -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOCPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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Database :

Issued Patents NA:
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	8	13.8	1438	3	US-08-434-099A-26	Sequence 26, Appl
2	8	13.8	10564	1	US-08-206-176-5	Sequence 5, Appl
3	7	12.1	711	4	US-09-543-681A-2950	Sequence 2950, Ap
4	7	12.1	1062	4	US-09-543-681A-1164	Sequence 1164, Ap
C 5	7	12.1	1509	4	US-09-134-000C-1868	Sequence 1868, Ap
C 6	7	12.1	1914	4	US-09-543-681A-2340	Sequence 2340, Ap
7	7	12.1	2082	4	US-09-543-681A-2670	Sequence 2670, Ap
C 8	7	12.1	2437	1	US-08-456-647B-3	Sequence 3, Appl
C 9	7	12.1	2437	2	US-08-237-401A-3	Sequence 3, Appl
C 10	7	12.1	2598	1	US-08-100-692-4	Sequence 4, Appl
C 11	7	12.1	2598	2	US-08-674-030-4	Sequence 4, Appl
C 12	7	12.1	2619	4	US-09-166-350-28	Sequence 28, Appl

7	12.1	2624	2	US-08-486-663A-17	Sequence 17, Appl
7	12.1	2624	3	US-08-247-904B-7	Sequence 7, Appl
7	12.1	2624	3	US-08-767-942A-20	Sequence 20, Appl
7	12.1	2625	6	US-08-435-637A-1	Sequence 1, Appl
7	12.1	3157	6	5198347-3	Patent No. 5198347
7	12.1	3321	1	US-08-484-438-5	Sequence 5, Appl
7	12.1	5484	3	US-09-633-580A-3	Sequence 3, Appl
7	12.1	5501	1	US-08-484-438-1	Sequence 1, Appl
7	12.1	5555	1	US-08-484-438-3	Sequence 3, Appl
7	12.1	9834	4	US-08-956-171E-37	Sequence 37, Appl
7	12.1	1830121	4	US-09-557-884-1	Sequence 1, Appl
7	12.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl
6	10.3	38	1	US-07-967-693-30	Sequence 30, Appl
6	10.3	38	1	US-08-195-072-28	Sequence 28, Appl
6	10.3	38	1	US-08-195-735-28	Sequence 28, Appl
6	10.3	38	1	US-08-195-747-28	Sequence 28, Appl
6	10.3	38	1	US-08-446-884-28	Sequence 28, Appl
6	10.3	38	1	US-08-195-073-28	Sequence 28, Appl
6	10.3	38	1	US-08-198-175-28	Sequence 28, Appl
6	10.3	38	2	US-08-443-153-28	Sequence 28, Appl
6	10.3	38	3	US-08-442-807-28	Sequence 28, Appl
6	10.3	38	3	US-08-856-331-17	Sequence 17, Appl
6	10.3	51	2	US-08-477-527A-71	Sequence 71, Appl
6	10.3	51	3	US-08-481-710-71	Sequence 71, Appl
6	10.3	51	5	PCT-US96-09537-71	Sequence 71, Appl
6	10.3	69	2	US-08-477-527A-33	Sequence 33, Appl
6	10.3	69	2	US-08-477-527A-39	Sequence 39, Appl
6	10.3	69	2	US-08-481-710-33	Sequence 33, Appl
6	10.3	69	3	US-08-481-710-34	Sequence 34, Appl
6	10.3	69	3	US-08-481-710-38	Sequence 38, Appl
6	10.3	69	5	PCT-US96-09537-33	Sequence 33, Appl
6	10.3	69	5	PCT-US96-09537-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-08-434-099A-26
; Sequence 26, Application US/08434099A
; Patent No. 6083902
; GENERAL INFORMATION:
; APPLICANT: Cedarholm-Wms., Stewart A.
; TITLE OF INVENTION: Recombinant Fibrin Chains,
; TITLE OF INVENTION: Fibrin and Fibrin-Homologs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.R. Squibb & Sons, Inc.
; STREET: 100 Headquarters Park Drive
; CITY: Skillman
; STATE: NJ
; COUNTRY: USA
; ZIP: 08558
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,099A
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/236,979
; FILING DATE: 02-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Jr., Esq., Theodore R
; REGISTRATION NUMBER: 30,942
; REFERENCE/DOCKET NUMBER: CV0054a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-281-2372
; TELEFAX: 908-281-2373
; TELEX:

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1438 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 3...1364
OTHER INFORMATION:
US-08-434-099A-26

Alignment Scores:
Pred. No.: 9.99 Length: 1438
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.79% Indels: 0
DB: 3 Gaps: 0

US-10-079-754A-10 (1-58) x US-08-434-099A-26 (1-1438)

QY 10 MetAlaLeuIleLeuAlaMetIle 17
DB 1003 ATGGCTTTGATTGGCGATGATC 1026

RESULT 2

US-08-206-176-5
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
FEATURE:
NAME/KEY: CDS
LOCATION: Join(1799...1876, 1973...2017, 2207...2390, 2510

LOCATION: ..2603, 4211...4341, 4645...4778, 5758...5942, 7426
LOCATION: ..7703, 9342...9571)
US-08-206-176-5

Alignment Scores:
Pred. No.: 63 Length: 10564
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.79% Indels: 0
DB: 1 Gaps: 0

US-10-079-754A-10 (1-58) x US-08-206-176-5 (1-10564)

QY 10 MetAlaLeuIleLeuAlaMetIle 17
DB 7524 ATGGCTTTGATTGGCGATGATC 7547

RESULT 3

US-09-543-681A-2950
Sequence 2950, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2950
LENGTH: 711
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-2950

Alignment Scores:
Pred. No.: 61.8 Length: 711
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 4 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-543-681A-2950 (1-711)

QY 8 PheIleMetAlaLeuIleLeu 14
DB 377 TTCATAATGCGATTGATTTG 397

RESULT 4

US-09-543-681A-1164
Sequence 1164, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1164
LENGTH: 1062
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-1164

Alignment Scores:

Pred. No.: 89.5 Length: 1062
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 4 Gaps: 0
US-10-079-754A-10 (1-58) x US-09-543-681A-1164 (1-1062)

Qy 8 PheleMetalaLeulleu 14
Db 467 TTTATTATGGCACTAATCCCTA 487

RESULT 5

US-09-134-000C-1868/c
; Sequence 1868, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1868
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1868

Alignment Scores:
Pred. No.: 124 Length: 1509
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 4 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-134-000C-1868 (1-1509)

Qy 3 llePhelePheValPheille 9
Db 1212 ATTTTATTTTGTTCATC 1192

RESULT 6

US-09-543-681A-2340/c
; Sequence 2340, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2340
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2340

Alignment Scores:
Pred. No.: 154 Length: 1914
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 12.07% Indels: 0
DB: 4 Gaps: 0
US-10-079-754A-10 (1-58) x US-09-543-681A-2340 (1-1914)

Qy 3 llePhelePheValPheille 9
Db 669 ATCTTCATCTCGTCTTCATC 649

RESULT 7

US-09-543-681A-2670/c
; Sequence 2670, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2670
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2670

Alignment Scores:
Pred. No.: 167 Length: 2082
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 4 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-543-681A-2670 (1-2082)

Qy 51 TyrProProAlaTyrProPhe 57
Db 1399 TACCCGCCAGCGTATCCATTT 1379

RESULT 8

US-08-456-647B-3/c
; Sequence 3, Application US/08456647B
; Patent No. 5811516
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,647B
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/237,401
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07251/007002
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; IMMEDIATE SOURCE:
; CLONE: Tyro-2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..2118
; US-08-456-647B-3
;
; Alignment Scores:
; Pred. No.: 193 Length: 2437
; Score: 7.00 Matches: 7
; Percent Similarity: 100.00% Conservative: 0
; Best Local Similarity: 100.00% Mismatches: 0
; Query Match: 12.07% Indels: 0
; DB: 1 Gaps: 0
;
; US-10-079-754A-10 (1-58) x US-08-456-647B-3 (1-2437)
;
; QY 13 lleleuAlaMetIleAtGAla 19
; DB 565 ATACTGCCATGATCAGAGCC 545
;
; RESULT 9
; US-08-237-401A-3/c
; Sequence 3, Application US/08237401A
; Patent No. 5837448
; GENERAL INFORMATION:
; APPLICANT: Lemke Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,401A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/884,486
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07251/007001
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1010...1321
; US-08-100-692-4
;
; Alignment Scores:
; Pred. No.: 204 Length: 2598
; Score: 7.00 Matches: 7
;
; US-10-079-754A-10 (1-58) x US-08-237-401A-3 (1-2437)
;
; QY 13 lleleuAlaMetIleAtGAla 19
; DB 565 ATACTGCCATGATCAGAGCC 545
;
; RESULT 10
; US-08-100-692-4/c
; Sequence 4, Application US/08100692
; Patent No. 5523448
; GENERAL INFORMATION:
; APPLICANT: Huibregtse, Jon M.
; APPLICANT: Scheffner, Martin
; APPLICANT: Howley, Peter M.
; TITLE OF INVENTION: E6 ASSOCIATED PROTEIN AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,692
; FILING DATE: 19930730
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-91
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2598 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1010...1321
; US-08-100-692-4
;
; Alignment Scores:
; Pred. No.: 204 Length: 2598
; Score: 7.00 Matches: 7

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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 12.07%              Indels: 0
DB: 1                             Gaps: 0

US-10-079-754A-10 (1-58) x US-08-100-692-4 (1-2598)

Qy      3 IlePheIlePheValPheIle 9
Db      543 ATCTTCATCTTTGTCTTCATC 523

RESULT 11
US-08-674-030-4/c
; Sequence 4, Application US/08674030
; Patent No. 5914389
; GENERAL INFORMATION:
; APPLICANT: Ruidregtse, Jon M.
; APPLICANT: Scheffner, Martin
; APPLICANT: Howley, Peter M.
; TITLE OF INVENTION: E6 ASSOCIATED PROTEIN AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,030
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,692
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-91
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2598 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1010..1321
; US-08-674-030-4

Alignment Scores:
Pred. No.: 204      Length: 2598
Score: 7.00         Matches: 7
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 12.07%              Indels: 0
DB: 2                Gaps: 0

US-10-079-754A-10 (1-58) x US-08-674-030-4 (1-2598)

Qy      3 IlePheIlePheValPheIle 9
Db      543 ATCTTCATCTTTGTCTTCATC 523
```

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RESULT 12
US-09-166-350-28/c
; Sequence 28, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Chen, Yao
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Old, Lloyd
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alex
; TITLE OF INVENTION: Renal Cancer Associated Antigens and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: L0461/7051
; CURRENT APPLICATION NUMBER: US/09/166,350A
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: US 09/166,350
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-166-350-28

Alignment Scores:
Pred. No.: 206      Length: 2619
Score: 7.00         Matches: 7
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 12.07%              Indels: 0
DB: 4                Gaps: 0

US-10-079-754A-10 (1-58) x US-09-166-350-28 (1-2619)

Qy      3 IlePheIlePheValPheIle 9
Db      564 ATCTTCATCTTTGTCTTCATC 544

RESULT 13
US-08-486-663A-17/c
; Sequence 17, Application US/08486663A
; Patent No. 5968761
; GENERAL INFORMATION:
; APPLICANT: Rolfe, Mark
; APPLICANT: Eckstein, Jens W.
; APPLICANT: Draetta, Giulio
; APPLICANT: Guillaume Cottarel
; TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,663A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-029CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2625
US-08-486-663A-17

Alignment Scores:
Pred. No.: 206 Length: 2624
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 2 Gaps: 0

US-10-079-754A-10 (1-58) x US-08-486-663A-17 (1-2624)

QY 3 llePheIlePheValPheIle 9
DB 543 ATCTTCATCTTGTTCATC 523

RESULT 14
US-08-247-904B-7/c
Sequence 7, Application US/08247904B
Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.01
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS

LOCATION: 1..2624
US-08-247-904B-7

Alignment Scores:
Pred. No.: 206 Length: 2624
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 2 Gaps: 0

US-10-079-754A-10 (1-58) x US-08-247-904B-7 (1-2624)

QY 3 llePheIlePheValPheIle 9
DB 543 ATCTTCATCTTGTTCATC 523

RESULT 15
US-08-767-942A-20/c
Sequence 20, Application US/08767942A
Patent No. 8068932
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 2624 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2622
US-08-767-942A-20

Alignment Scores:
Pred. No.: 206 Length: 2624
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.07% Indels: 0
DB: 3 Gaps: 0

US-10-079-754A-10 (1-58) x US-08-767-942A-20 (1-2624)

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Run on: August 16, 2004, 01:12:59 ; Search time 326 Seconds

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Title: US-10-079-754A-10

Perfect score: 58

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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
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RESULT 1
US-10-079-754A-15
; Sequence 15, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15

ALIGNMENTS

1	58	100.0	267	14	US-10-079-754A-15	Sequence 15, Appl
2	58	100.0	267	14	US-10-079-623-200	Sequence 200, App
3	58	100.0	505	14	US-10-079-754A-1	Sequence 1, Appli
4	58	100.0	604	14	US-10-079-754A-4	Sequence 4, Appli
5	51	87.9	585	14	US-10-079-754A-2	Sequence 2, Appli
6	34	58.6	525	14	US-10-079-754A-6	Sequence 6, Appli
7	27	46.6	869	14	US-10-079-754A-3	Sequence 3, Appli
8	11	19.0	96	14	US-10-079-754A-5	Sequence 5, Appli
C 9	9	15.5	7726	13	US-09-812-350-48	Sequence 48, Appl
C 10	8	13.8	181	13	US-09-918-995-8815	Sequence 8815, Ap
C 11	8	13.8	339	13	US-10-424-599-92870	Sequence 92870, A
C 12	8	13.8	390	10	US-09-918-995-8225	Sequence 8225, Ap
C 13	8	13.8	464	10	US-09-918-995-8118	Sequence 8118, Ap
C 14	8	13.8	808	17	US-10-437-963-56029	Sequence 56029, A
C 15	8	13.8	870	15	US-10-198-846-5963	Sequence 5963, Ap
C 16	8	13.8	1485	13	US-10-425-114-31277	Sequence 31277, A
C 17	8	13.8	1605	15	US-10-198-846-13051	Sequence 13051, A
C 18	8	13.8	12072	17	US-10-283-975A-255	Sequence 255, App
C 19	7	12.1	261	17	US-10-437-963-67969	Sequence 67969, A
C 20	7	12.1	320	9	US-09-962-832-138	Sequence 138, App
C 21	7	12.1	320	9	US-09-954-531-1010	Sequence 1010, Ap
C 22	7	12.1	342	17	US-10-437-963-39267	Sequence 39267, A
C 23	7	12.1	349	9	US-09-770-791-721	Sequence 721, App
C 24	7	12.1	349	13	US-10-282-122A-16688	Sequence 16688, A
C 25	7	12.1	357	17	US-10-437-963-31469	Sequence 91469, A
C 26	7	12.1	358	9	US-09-917-800A-522	Sequence 522, App
C 27	7	12.1	358	12	US-10-152-319A-585	Sequence 585, App
C 28	7	12.1	358	16	US-10-191-803-1105	Sequence 1105, Ap
C 29	7	12.1	364	10	US-09-873-367C-617	Sequence 617, App
C 30	7	12.1	369	13	US-10-424-599-40304	Sequence 40304, A
C 31	7	12.1	412	9	US-09-860-670-20	Sequence 20, Appl
C 32	7	12.1	412	16	US-10-227-646-20	Sequence 20, Appl
C 33	7	12.1	427	9	US-09-960-352-10246	Sequence 10246, A
C 34	7	12.1	454	13	US-10-424-599-114944	Sequence 114944, A
C 35	7	12.1	457	17	US-10-115-635-304	Sequence 304, App
C 36	7	12.1	485	10	US-09-918-995-32017	Sequence 32017, A
C 37	7	12.1	500	10	US-09-991-936-148	Sequence 148, App
C 38	7	12.1	509	13	US-10-424-599-36128	Sequence 36128, A
C 39	7	12.1	520	13	US-10-027-632-60602	Sequence 60602, A
C 40	7	12.1	520	13	US-10-027-632-60603	Sequence 60603, A
C 41	7	12.1	520	13	US-10-027-632-61489	Sequence 61489, A
C 42	7	12.1	520	13	US-10-027-632-61490	Sequence 61490, A
C 43	7	12.1	520	13	US-10-027-632-61688	Sequence 61688, A
C 44	7	12.1	520	13	US-10-027-632-61689	Sequence 61689, A
C 45	7	12.1	520	13	US-10-027-632-62287	Sequence 62287, A

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15
LENGTH: 267
TYPE: DNA
ORGANISM: Bovine
US-10-079-754A-15

Alignment Scores:

Pred. No.: 9,01e-54 Length: 267
Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-15 (1-267)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaASP 20
DB 44 ATGAAGATCTTTATCTTTGCTCTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
DB 104 TCATCTGAAGAGAACGTCACAGGAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217

RESULT 2

US-10-079-623-200

Sequence 200, Application US/10079623
Publication No. US20020169302A1
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions isolated from bovine
FILE REFERENCE: 11000.1044c3
CURRENT APPLICATION NUMBER: US/10/079,623
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 370
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 200
LENGTH: 267
TYPE: DNA
ORGANISM: Bovine
US-10-079-623-200

Alignment Scores:

Pred. No.: 9,01e-54 Length: 267
Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-623-200 (1-267)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaASP 20
DB 44 ATGAAGATCTTTATCTTTGCTCTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
DB 104 TCATCTGAAGAGAACGTCACAGGAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217

RESULT 3

US-10-079-754A-1

Sequence 1, Application US/10079754A
Publication No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60,150,330
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 505
TYPE: DNA
ORGANISM: Bovine
US-10-079-754A-1

Alignment Scores:

Pred. No.: 1.66e-53 Length: 505
Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-1 (1-505)

QY 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaASP 20
DB 44 ATGAAGATCTTTATCTTTGCTCTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGAT 103
QY 21 SerSerGluGluLysArgHisArgLysArgLysLysHisHisArgGlyTyrPheGlnGln 40
DB 104 TCATCTGAAGAGAACGTCACAGGAACGGAACCAACATCATAGAGGATATTTTCAACAA 163
QY 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
DB 164 TACCAGCCATATCAACGATATCCATAAATATCTCTCGGTATCCATTTCCT 217

RESULT 4

US-10-079-754A-4

Sequence 4, Application US/10079754A
Publication No. US20020164625A1
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Davis, Stephen R.
TITLE OF INVENTION: Compositions Isolated from Bovine
FILE REFERENCE: 11000.1068
CURRENT APPLICATION NUMBER: US/10/079,754A
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/699,146
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60,162,701
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 09/644,190
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60,150,330

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; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-4

Alignment Scores:
Pred. No.: 1.97e-53 Length: 604
Score: 58.00 Matches: 58
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-4 (1-604)

Qy 1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
Db 154 ATGAAGATCTTTATCTTGTCTTCATTCCTCCTAGCCATGATTAGAGCTGAT 213
Qy 21 SerSerGluGluLysArgHisArgLysArgLysHisArgLysHisArgLysHisArgLysHis 40
Db 214 TCATCTGAAGAGAAACGTACAGGAAACGGGAAACATCATAGAGATATTTTCAACAA 273
Qy 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProAlaTyrProPhePro 58
Db 274 TACCAGCATATCAACGATATCCACTAAATATCTCTCTGGTATCCATTTCTCT 327

RESULT 5
US-10-079-754A-2
; Sequence 2, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-5

Alignment Scores:
Pred. No.: 1.5e-27 Length: 525
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 58.62% Indels: 0
DB: 14 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-079-754A-6 (1-525)

Qy 1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
Db 43 ATGAAGATCTTTATCTTGTCTTCATTCCTCCTAGCCATGATTAGAGCTGAT 102
Qy 21 SerSerGluGluLysArgHisArgLysArgLysHisHisHis 34
Db 103 TCATCTGAAGAGAAACGTACAGGAAACGGGAAACATCAT 144

RESULT 7
US-10-079-754A-3
; Sequence 3, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146

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DB: 10 Gaps: 0
US-10-079-754A-10 (1-58) x US-09-918-995-8815 (1-181)

QY 10 MetAlaLeuIleLeuAlaMetIle 17
|||||
DB 92 ATGGCTTTGATTTCGGCGATGATC 115

RESULT 11

US-10-424-599-92870/c
; Sequence 92870, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David X
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285694
; SEQ ID NO 92870
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54877C.1
US-10-424-599-92870

Alignment Scores:
Pred. No.: 12.5 Length: 339
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.79% Indels: 0
DB: 13 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-424-599-92870 (1-339)

QY 16 MetIleArgAlaAspSerSerGlu 23
|||||
DB 225 ATGATCCGCGCAGACTCGAGTGAG 202

RESULT 12

US-09-918-995-8225
; Sequence 8225, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8225
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-8225

Alignment Scores:
Pred. No.: 14.3 Length: 390
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.79% Indels: 0
DB: 10 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-918-995-8225 (1-390)
QY 10 MetAlaLeuIleLeuAlaMetIle 17
|||||
DB 137 ATGGCTTTGATTTCGGCGATGATC 160

RESULT 13

US-09-918-995-8118
; Sequence 8118, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8118
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(464)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-8118

Alignment Scores:
Pred. No.: 16.9 Length: 464
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.79% Indels: 0
DB: 10 Gaps: 0

US-10-079-754A-10 (1-58) x US-09-918-995-8118 (1-464)

QY 10 MetAlaLeuIleLeuAlaMetIle 17
|||||
DB 254 ATGGCTTTGATTTCGGCGATGATC 277

RESULT 14

US-10-437-963-56029/c
; Sequence 56029, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 56029
; LENGTH: 808
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57980C.1
US-10-437-963-56029

Alignment Scores: Length: 808
 Pred. No.: 28.8 Matches: 8
 Score: 8.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 13.79%
 DB: 17
 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-437-963-56029 (1-808)

QY 11 AlalaLeuIleAlaMetIleArg 18
 DB 90 GCCTCATCTTGGCTATGATCAGG 67

RESULT 15

US-10-198-846-5963/c
 ; Sequence 5963, Application US/10198846
 ; Publication No. US20030099974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lillie, James
 ; APPLICANT: Xu, Yongyao
 ; APPLICANT: Wang, Youzhen
 ; APPLICANT: Steinmann, Kathleen
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF BREAST CANCER
 ; FILE REFERENCE: MRI-049
 ; CURRENT APPLICATION NUMBER: US/10/198,846
 ; CURRENT FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/306,220
 ; PRIOR FILING DATE: 2001-07-18
 ; NUMBER OF SEQ ID NOS: 14084
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5963
 ; LENGTH: 870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 26, 412, 496, 541, 543, 646, 649, 653, 711, 730, 742, 764,
 ; LOCATION: 768, 779, 781, 785, 795, 800, 804, 809, 811, 821, 823, 829,
 ; LOCATION: 830, 832, 839, 851, 853, 866, 870
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-198-846-5963

Alignment Scores: Length: 870
 Pred. No.: 30.9 Matches: 8
 Score: 8.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 13.79%
 DB: 15
 Gaps: 0

US-10-079-754A-10 (1-58) x US-10-198-846-5963 (1-870)

QY 10 MetAlaLeuIleLeuAlaMetIle 17
 DB 121 ATGGCTTTGATTGGCGATGATC 98

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 Job time : 329 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: August 6, 2004, 17:10:01 ; Search time 22 Seconds
without alignments)
2834.735 Million cell updates/sec

Title:
Perfect score: 1029
Sequence: 1 gaagattttcagttctata.....tatcaagcataaaaaaaa 604

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Missing first 45 summaries

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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct THR_MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10079754 @CGN 1.1 27 @runat_06082004_180756_1728 -NCPUS=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A.COMB.pcp:*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pcp:*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pcp:*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pcp:*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pcp:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
C 1	75	7.2	370 1 US-08-415-818-12 Sequence 12, Appl
C 2	75	7.2	370 2 US-08-894-236-12 Sequence 12, Appl
C 3	75	7.2	370 5 PCT-US96-01444-12 Sequence 12, Appl
C 4	73.5	7.1	1312 4 US-09-495-714C-2 Sequence 2, Appl
C 5	73.5	7.1	1977 4 US-09-495-714C-4 Sequence 4, Appl
C 6	72.5	7.0	1985 4 US-09-495-714C-6 Sequence 6, Appl
C 7	70	6.8	233 4 US-09-489-847-176 Sequence 176, App
C 8	69.5	6.8	273 4 US-09-252-991A-19818 Sequence 19818, A
C 9	68.5	6.6	273 4 US-08-936-165A-395 Sequence 395, App
C 10	68	6.6	482 4 US-09-107-532A-5672 Sequence 5672, Ap
C 11	67.5	6.6	926 1 US-08-159-340A-2 Sequence 2, Appl
C 12	66.5	6.5	161 2 US-08-286-819A-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-415-818-12
; Sequence 12, Application US/08415818
; Patent No. 5621079
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,818
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087

13	66.5	6.5	161	3	US-08-980-357-25	Sequence 25, Appl
C 14	66.5	6.4	317	4	US-09-393-634-60	Sequence 60, Appl
15	66	6.4	396	4	US-09-079-030-219	Sequence 219, App
16	66	6.4	1056	4	US-09-079-030-217	Sequence 217, App
17	66	6.4	4536	4	US-09-180-422B-27	Sequence 27, Appl
18	66	6.4	4536	4	US-09-079-030-1	Sequence 1, Appl
19	66	6.4	4563	4	US-09-108-006C-1	Sequence 1, Appl
C 20	65	6.3	247	4	US-09-134-000C-5222	Sequence 5222, Ap
C 21	65	6.3	371	1	US-08-415-818-6	Sequence 6, Appl
C 22	65	6.3	371	2	US-08-894-236-6	Sequence 4, Appl
C 23	65	6.3	371	2	US-08-919-624-4	Sequence 6, Appl
C 24	65	6.3	371	5	PCT-US96-01444-6	Sequence 5146, Ap
C 25	64.5	6.2	62	4	US-09-134-001C-5146	Sequence 1, Appl
26	64.5	6.2	1608	4	US-09-568-407-1	Sequence 1244, Ap
27	64	6.2	160	4	US-09-198-452A-1244	Sequence 8193, Ap
28	64	6.2	491	4	US-09-489-039A-8193	Sequence 356, App
29	63.5	6.2	115	3	US-08-513-974B-356	Sequence 26, Appl
30	63.5	6.2	117	3	US-09-073-297-26	Sequence 2, Appl
31	63.5	6.2	124	1	US-08-307-499-2	Sequence 2, Appl
32	63.5	6.2	124	3	US-09-299-268-2	Sequence 20066 A
C 33	63.5	6.1	268	4	US-09-252-991A-20066	Sequence 13, Appl
34	63.5	6.2	348	1	US-08-118-270-13	Sequence 13, Appl
35	63.5	6.2	348	5	PCT-US93-08528-13	Sequence 7127, Ap
36	63.5	6.2	526	4	US-09-107-532A-7127	Sequence 3464, Ap
37	63.5	6.2	2404	4	US-09-134-001C-3464	Sequence 6911, Ap
C 38	63	6.1	177	4	US-09-107-532A-5911	Sequence 8, Appl
39	63	6.1	182	1	US-07-962-569A-8	Sequence 2, Appl
40	63	6.1	182	1	US-08-308-883-2	Sequence 2, Appl
41	63	6.1	182	1	US-08-730-163-2	Sequence 2, Appl
42	63	6.1	182	3	US-08-256-799-2	Sequence 2, Appl
43	63	6.1	182	3	US-08-462-437-2	Sequence 2, Appl
44	63	6.1	182	3	US-08-462-437-31	Sequence 31, Appl
45	63	6.1	346	3	US-09-073-297-2	Sequence 2, Appl

REFERENCE/DOCKET NUMBER: 19390
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3462
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 370 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-415-818-12

Alignment Scores:
 Pred. No.: 0.892 Length: 370
 Score: 75.00 Matches: 49
 Percent Similarity: 35.51% Conservative: 27
 Best Local Similarity: 22.90% Mismatches: 70
 Query Match: 7.23% Indels: 68
 DB: 1 Gaps: 13

US-10-079-754A-4 (1-604) x US-08-415-818-12 (1-370)

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QY 564 ATGGTAAGTACAGAGAAAGAGTAGAA-----ACCAATTACATAGTTCAGAGACTA 511
Db 59 llellePheLysLysGlnArgLysAlaGlnAsnPheThrSerlleLeulleAlaAsnLeu 78
QY 510 TCA-----TTATTATGTTTTAAATATATTGATTTCCTCAAGTATGTTG 463
Db 79 SerLeuSerAspThrLeuValCysValMetCysIleHisPheThrIlelleTyrThrLeu 98
QY 462 TCGAACTAC-----TTGACTGATTTTTTTTCTTTCTTTGTT 430
Db 99 MetAspHisTrpIlePheGlyAspThrMetCysArgLeuThrSerTyrValGlnSerVal 118
QY 429 -----TTATTCAATTGAAAGATGTTTTTCAACACAGAGAGTAGGAAAATC 379
Db 119 SerlleSerValSerllePheSerLeuValPheThrAlaValGluArgTyrGlnLeulle 138
QY 378 ATT-----GTGAAAATCTCTCTAATCATGTCCTGTAGTTACTAAGCAGCATT 331
Db 139 ValAsnProArgGlyTrpLysProSerValThrHisAlaTyr----- 152
QY 330 TTAAGGAATGATACGAGCAGGAGTAATTAGTGG--ATATCGTTGATATGCTGGTA 274
Db 153 -----TrpGlylleThrLeulleIleTrpLeuPhe 161
QY 273 TTGTTGAAATATCTCTATGATGTTTTTTCGTTTCTGTGACGTTTCTCTTCAGATGA 214
Db 162 SerLeuLeuLeuSerllePhePheLeuSerTyrHisLeuThr----- 176
QY 213 ATCAGCTTATCATGCTAGATGAGCAGC---CATATGAAGACAAAGATAAGATCTT 157
Db 177 -----AspGluProPheHisAsnLeuSerLeuProThrAspLeu 189
QY 156 CATATT-----TGGTGGAGTCCAGTCATGAAAGATGAAATT 121
Db 190 TyrThrHisGlnValAlaCysValGluAsnTrp-----ProSerLysLysAspArgLeu 207
QY 120 CTGATGCTTACGAGATGTTCTTTGCTAGAAAACGCTGCTGTTTAAATACCTTGAATCC 61
Db 208 LeuPheThrThrSerLeuPheLeuGlnTyrPheValProLeu-----Gly 223
QY 60 TTCATTTCTTTTGTAAATTACATCAGTTATGAGATCTTATTA 19
Db 224 PheilleulleCys---TyrLeuLyslleValilleCysLeu 236

```

RESULT 2

US-08-894-236-12
 Sequence 12, Application US/08894236
 Patent No. 5939263
 GENERAL INFORMATION:
 APPLICANT: Cascieri, Margaret A.

APPLICANT: Linemeyer, David L.
 APPLICANT: MacNeil, Douglas J.
 APPLICANT: Shiao, Lin-Lin
 APPLICANT: Strader, Catherine D.
 APPLICANT: Tan, Carina P.
 APPLICANT: Weinberg, David H.
 TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mary A. Appollina
 STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 CITY: Rahway
 STATE: NJ
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/894,236
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/383,746
 FILING DATE: 03-FEB-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/415,818
 FILING DATE: 03-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Appollina, Mary A.
 REGISTRATION NUMBER: 34,087
 REFERENCE/DOCKET NUMBER: 19390Y
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3462
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 370 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-894-236-12

Alignment Scores:
 Pred. No.: 0.892 Length: 370
 Score: 75.00 Matches: 49
 Percent Similarity: 35.51% Conservative: 27
 Best Local Similarity: 22.90% Mismatches: 70
 Query Match: 7.23% Indels: 68
 DB: 2 Gaps: 13

US-10-079-754A-4 (1-604) x US-08-894-236-12 (1-370)

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QY 564 ATGGTAAGTACAGAGAAAGAGTAGAA-----ACCAATTACATAGTTCAGAGACTA 511
Db 59 llellePheLysLysGlnArgLysAlaGlnAsnPheThrSerlleLeulleAlaAsnLeu 78
QY 510 TCA-----TTATTATGTTTTAAATATATTGATTTCCTCAAGTATGTTG 463
Db 79 SerLeuSerAspThrLeuValCysValMetCysIleHisPheThrIlelleTyrThrLeu 98
QY 462 TCGAACTAC-----TTGACTGATTTTTTTTCTTTCTTTGTT 430
Db 99 MetAspHisTrpIlePheGlyAspThrMetCysArgLeuThrSerTyrValGlnSerVal 118
QY 429 -----TTATTCAATTGAAAGATGTTTTTCAACACAGAGAGTAGGAAAATC 379
Db 119 SerlleSerValSerllePheSerLeuValPheThrAlaValGluArgTyrGlnLeulle 138
QY 378 ATT-----GTGAAAATCTCTCTAATCATGTCCTGTAGTTACTAAGCAGCATT 331

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Db 139 ValAsnProArgGlyTyrLysProSerValThrHisAlaTyr-----152.
Qy 330 TTAAGGAATGGATACACAGAGAGATAATTTAGTGG--ATATCGTTGATATGCTGGTA 274
Db 153 -----TrrpGlyIleThrLeuIleThrLeuPhe 161
Qy 273 TTGTTGAAATATCTCTATGATGTTTTCCTGCTGAGGTTTCTCTTCAGATGA 214
Db 162 SerLeuLeuSerIleProPhePheLeuSerTyrHisLeuThr-----176
Qy 213 ATCAGCTCTAATCATGCTAGGATGAGAGC---CATATGAAGACAAAGATAAGATCTT 157
Db 177 -----AspGluProPheHisAsnLeuSerLeuProThrAspLeu 189
Qy 156 CATATT-----TGGTGGAGTCCAGTCATGAAAGATGAAATT 121
Db 190 TyrThrHisGlnValAlaCysValGluAsnTrp-----ProSerLysLysAspArgLeu 207
Qy 120 CTGATGCTTCAGGAGATGTTCTTTGCTAGAAACTGCTGTTGTTTAAATACCTTGAATCC 61
Db 208 LeuPheThrThrSerLeuPheLeuGlnTyrPheValProLeu-----Gly 223
Qy 60 TTCATTGCTTTTCTTAATCATCATGATGATGATGATCTTATTA 19
Db 224 PheIleLeuIleCys---TyrLeuLysIleValIleCysLeu 236
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RESULT 3

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PCT-US96-01444-12
; Sequence 12, Application PC/TUS9601444
; GENERAL INFORMATION:
; APPLICANT: Cascieri, Margaret A.
; APPLICANT: Linemeyer, David L.
; APPLICANT: MacNeil, Douglas J.
; APPLICANT: Shiao, Lin-Lin
; APPLICANT: Strader, Catherine D.
; APPLICANT: Tan, Carina P.
; APPLICANT: Weinberg, David H.
; TITLE OF INVENTION: NEUROPEPTIDE Y RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary A. Appollina
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01444
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/383,746
; FILING DATE: 03-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/415,818
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19390Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3462
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01444-12
Alignment Scores:
Pred. No.: 0.892 Length: 370
Score: 75.00 Matches: 49
Percent Similarity: 35.51% Conservative: 27
Best Local Similarity: 22.90% Mismatches: 70
Query Match: 7.23% Indels: 68
DB: 5 Gaps: 13
US-10-079-754A-4 (1-604) x PCT-US96-01444-12 (1-370)
Qy 564 ATGTAAGTCAGACAGAAAGAAAGTAGAA-----ACCAATTACATAGTTCAGAGACTA 511
Db 59 IleIlePheLysLysGlnArgLysAlaGlnAsnPheThrSerIleLeuIleAlaAsnLeu 78
Qy 510 TCA-----TTATTATGTTTTTAAATATTGATATTTCATCCAAAGTATGTTG 463
Db 79 SerLeuSerAspThrLeuValCysValMetCysIleHisPheThrIleIleTyrThrLeu 98
Qy 462 TGCACTAC-----TTGACTGATTTTTTTTTTCTTTCTTTGTT 430
Db 99 MetAspHisTrpIlePheGlyAspThrMetCysArgLeuThrSerTyrValGlnSerVal 118
Qy 429 -----TTATTCAATTTGAAGATGTTTTCACACACACAGAAAGAGTAGGAAAAATC 379
Db 119 SerIleSerValSerIlePheSerLeuValPheThrAlaValGluArgTyrGlnLeuIle 138
Qy 378 ATT-----GTGAAAAATCTCTCTAATCATGCTCTCTAGTACTAAGCAGCATT 331
Db 139 ValAsnProArgGlyTrpLysProSerValThrHisAlaTyr-----152
Qy 330 TTAAGGAATGGATACACAGGAGGATAATTTAGTGG--ATATCGTTGATATGCTGGTA 274
Db 153 -----TrpGlyIleThrLeuIleThrLeuPhe 161
Qy 273 TTGTTGAAATATCTCTATGATGTTTTCCTGCTGACGTTTCTCTTCAGATGA 214
Db 162 SerLeuLeuLeuSerIleProPhePheLeuSerTyrHisLeuThr-----176
Qy 213 ATCAGCTCTAATCATGCTAGGATGAGAGC---CATATGAAGACAAAGATAAGATCTT 157
Db 177 -----AspGluProPheHisAsnLeuSerLeuProThrAspLeu 189
Qy 156 CATATT-----TGGTGGAGTCCAGTCATGAAAGATGAAATT 121
Db 190 TyrThrHisGlnValAlaCysValGluAsnTrp-----ProSerLysLysAspArgLeu 207
Qy 120 CTGATGCTTCAGGAGATGTTCTTTGCTAGAAACTGCTGTTTAAATACCTTGAATCC 61
Db 208 LeuPheThrThrSerLeuPheLeuGlnTyrPheValProLeu-----Gly 223
Qy 60 TTCATTGCTTTTCTTAATCATCATGATGATGATGATCTTATTA 19
Db 224 PheIleLeuIleCys---TyrLeuLysIleValIleCysLeu 236
RESULT 4
US-09-495-714C-2
; Sequence 2, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1912
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2

Alignment Scores:
Pred. No.: 1.94 Length: 1912
Score: 73.50 Matches: 32
Percent Similarity: 42.31% Conservative: 23
Best Local Similarity: 24.62% Mismatches: 46
Query Match: 7.09% Indels: 29
DB: 4 Gaps: 6

US-10-079-754A-4 (1-604) x US-09-495-714C-2 (1-1912)
QY 369 AATCTCTTAATCATGCTCTAGTACTAAGCAGCATTTTAAAGAAATGATACGCAGG 310
Db 576 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerIleAlaSer 593
QY 309 AGGATAATTTAGTGATATCGTTGATATCGTGTGATATGTTGTAATAATCTCTATGATG 250
Db 594 LeuLeuLeu-----LeuLeuPheLeuPheIleIlePheSerLeuLeuGlyMetGln 611
QY 249 TTTTTCGCTTCTGTCAGCTTCTCTTCAGATGAATCAGCTCTAATCATGGCTAGGAT 190
Db 612 LeuPheGlyGlyLysPheAsnPhe-----Asp 620
QY 189 GAGAGCCATAATGAAGACAAAGATAAAGAT-----CTTCATATTGG 148
Db 621 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 640
QY 147 -----TGGAGTCCAGTCATGAAGATGAATCTCTCATGCTTCAG 109
Db 641 GlnIleLeuThrGlyGluAspTrpAsnValMetTyrAspGlyIleMetAlaTyrGly 660
QY 108 GAGATGTTCTTTGCTAGAAAACGCTGTGTTAAATACCTTGAAATCCTTCATTGTTTT 49
Db 661 GlyProPhePheProGlyMetLeuValCysIleTyrPheIleIleLeuPheIleCys--- 679
QY 48 TGTAAATTACATCAGTTATGAGATCTTATTA 19
Db 680 GlyAsnTyrIleLeuLeuAsnValPheLeu 689

RESULT 5
; Sequence 4, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-4

Alignment Scores:
Pred. No.: 1.95 Length: 1977
Score: 73.50 Matches: 32
Percent Similarity: 42.31% Conservative: 23
Best Local Similarity: 24.62% Mismatches: 46
Query Match: 7.09% Indels: 29
DB: 4 Gaps: 6

US-10-079-754A-4 (1-604) x US-09-495-714C-4 (1-1977)
QY 369 AATCTCTTAATCATGCTCTAGTACTAAGCAGCATTTTAAAGAAATGATACGCAGG 310
Db 641 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerIleAlaSer 658

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-495-714C-6

Alignment Scores:
Pred. No.: 2.59 Length: 1985
Score: 72.50 Matches: 32
Percent Similarity: 42.31% Conservative: 23
Best Local Similarity: 24.62% Mismatches: 46
Query Match: 6.99% Indels: 29
DB: 4 Gaps: 6

US-10-079-754A-4 (1-604) x US-09-495-714C-6 (1-1985)
QY 369 AATCTCTTAATCATGCTCTAGTACTAAGCAGCATTTTAAAGAAATGATACGCAGG 310
Db 641 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerIleAlaSer 658
QY 309 AGGATAATTTAGTGATATCGTTGATATCGTGTGATATGTTGTAATAATCTCTATGATG 250
Db 659 LeuLeuLeu-----LeuLeuPheLeuPheIleIlePheSerLeuLeuGlyMetGln 676
QY 249 TTTTTCGCTTCTGTCAGCGTTTCTCTTCAGATGAATCAGCTCTAATCATGGCTAGGAT 190
Db 677 LeuPheGlyGlyLysPheAsnPhe-----Asp 685
QY 189 GAGAGCCATAATGAAGACAAAGATAAAGAT-----CTTCATATTGG 148
Db 686 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 705
QY 147 -----TGGAGTCCAGTCATGAAGATGAATCTCTCATGCTTCAG 109
Db 706 GlnIleLeuThrGlyGluAspTrpAsnValMetTyrAspGlyIleMetAlaTyrGly 725

RESULT 6
; Sequence 6, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1985
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-495-714C-6

Alignment Scores:
Pred. No.: 2.59 Length: 1985
Score: 72.50 Matches: 32
Percent Similarity: 42.31% Conservative: 23
Best Local Similarity: 24.62% Mismatches: 46
Query Match: 6.99% Indels: 29
DB: 4 Gaps: 6

US-10-079-754A-4 (1-604) x US-09-495-714C-6 (1-1985)
QY 369 AATCTCTTAATCATGCTCTAGTACTAAGCAGCATTTTAAAGAAATGATACGCAGG 310
Db 641 SerLeuSerAsnLeuValAlaSerLeuLeuAsnSerMet-----LysSerIleAlaSer 658
QY 309 AGGATAATTTAGTGATATCGTTGATATCGTGTGATATGTTGTAATAATCTCTATGATG 250
Db 659 LeuLeuLeu-----LeuLeuPheLeuPheIleIlePheSerLeuLeuGlyMetGln 676
QY 249 TTTTTCGCTTCTGTCAGCGTTTCTCTTCAGATGAATCAGCTCTAATCATGGCTAGGAT 190
Db 677 LeuPheGlyGlyLysPheAsnPhe-----Asp 685
QY 189 GAGAGCCATAATGAAGACAAAGATAAAGAT-----CTTCATATTGG 148
Db 686 GlnThrHisThrLysArgSerThrPheAspThrPheProGlnAlaLeuLeuThrValPhe 705
QY 147 -----TGGAGTCCAGTCATGAAGATGAATCTCTCATGCTTCAG 109
Db 706 GlnIleLeuThrGlyGluAspTrpAsnValMetTyrAspGlyIleMetAlaTyrGly 725

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; Sequence 395, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: NO. 6348582a1 Prokaryotic Polynucleotides,
; POLYPEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936.165A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,032
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 395:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-936-165A-395

Alignment Scores:
Pred. No.: 5.28 Length: 273
Score: 68.50 Matches: 23
Percent Similarity: 40.66% Conservative: 14
Best Local Similarity: 25.27% Mismatches: 24
Query Match: 6.61% Indels: 30
DB: 4 Gaps: 3

US-10-079-754A-4 (1-604) x US-08-936-165A-395 (1-273)
QY 285 ATATGGCTGGTATGTTGAAATATCTCTATGATGTTTTCGGTTTCTGTGACGTTT 226
Db 61 IleIrpSerAsnPheIleGluMetGlySerMetMetLeuLeuProMetSerMetLeuPhe 80
QY 225 CTCTTCAGATGAATCAGCTCTAATCATGGCTAGGATGAGGCCATATGAGACAAAGAT 166
Db 81 LeuPheGlyArgMetLeuSerArgHisGly 90
QY 165 AAAGATCTTCATATTTGGTGGAGTCCAGTCATGATGAAGATGAATTCGTGCTTCAGGAG 106
Db 91 LysArgValHis 103

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QY 105 ATGTTCTTTTGTAGAAAACACTGCTGTGTTTAAATACCTTGAATCCTTCATTGTTTGT 46
Db 104 MetPhePhe-Ile-PhelIleAlaIle 111
QY 45 AATTACATCAGTTATGAGATCTTATTATAGA 15
Db 111 eLeuThrLeuThrMetTrpSerGluTyrArg 121

RESULT 10
US-09-107-532A-5672
; Sequence 5672, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5672:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 482 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...482
; SEQUENCE DESCRIPTION: SEQ ID NO: 5672:
US-09-107-532A-5672

Alignment Scores:
Pred. No.: 6.87 Length: 482
Score: 68.00 Matches: 31
Percent Similarity: 43.54% Conservative: 33
Best Local Similarity: 21.09% Mismatches: 41
Query Match: 6.56% Indels: 42
DB: 4 Gaps: 7

US-10-079-754A-4 (1-604) x US-09-107-532A-5672 (1-482)
QY 546 AAGAAAGTAGAAACCAATTACATGATTCAGACA----- 514
Db 167 GlnAsnLeuLysPheAsnTyrLysMetGlnGlnTyrPheValPheThrLeuIlePhe 186

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QY 513 -----CTATCATATTATGTTTAAATATTGATATTGATTTCAAGTATGTTGTGC 460
 Db 187 SerllelethrPheMetPheArgPheGluTyrPheThrThrArgTyrThrTyrSer 206
 QY 459 AACTACTGTAGTGAATTTTCTTTGTTTATTTATTCATTTGAAAGATGGTTTCAACACA 400
 Db 207 AsnLeullethrAsnSerSerLeuTyrLeullePhe-----PheSerAla 221
 QY 399 ACAGAAAGAGTA-----GGAAATCATTTGTG-----AAAAATCTCTCTAATCAT 355
 Db 222 ThrLysGlylleAlaThrAlaSerLeulleMetGluAlaGlnLysPheLeuThrHisHis 241
 QY 354 GTC-----CTGTAGTTACTAAGCAGCATTTTA----- 328
 Db 242 LysAsnleleArgArgLeuLeuValSerSerPheLeuPheleTyrAsnValAsnProPhe 261
 QY 327 -----AGAAATGGATACGACGAGGAGATATTTAGTGATATCGTTGATATGGCTG 277
 Db 262 AsnValSerArgTyrTyrIleSerTyrValValleLeuPheMetLeullePhePheThr 281
 QY 276 GTATTGTTGAAATATCTCTCATG-----ATGTTTCTTCCGTTT 238
 Db 282 LysLyslleLysValAsnGlnMetLeulleLeulleLeuGlyMetPhePhelePhe 301
 QY 237 CCTGTGAGCTTTCTCTCAGA 217
 Db 302 ProLeuLeuAsnPhePheArg 308

RESULT 11

US-08-159-340A-2
 ; Sequence 2, Application US/08159340A
 ; Patent No. 5565352
 ; GENERAL INFORMATION:
 ; APPLICANT: Hochstrasser, Mark
 ; APPLICANT: Papa, Ferroz
 ; TITLE OF INVENTION: DEUBICUITINATING ENZYME: COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/159,340A
 ; FILING DATE: 24-NOV-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Highlander, Steven L.
 ; REGISTRATION NUMBER: 37,642
 ; REFERENCE/DOCKET NUMBER: AKCD:112/HYL
 ; TELEPHONE: (512) 418-3000
 ; TELEFAX: (512) 474-7577
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 926 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-159-340A-2
 ; Alignment Scores:
 ; Pred. No.: 9.1 Length: 926

Score: 67.50 Matches: 48
 Percent Similarity: 39.11% Conservative: 22
 Best Local Similarity: 26.82% Mismatches: 51
 Query Match: 6.56% Indels: 58
 DB: 1 Gaps: 10

US-10-079-754A-4 (1-604) x US-08-159-340A-2 (1-926)

QY 82 CAGCAGTCTTTAGCAAGAAACATCTCTGAGCATCAGAATTC-----ATCTTT 132
 Db 390 GlnGlnSerAspAsnAspHisValLeuLysArgSerSerPheLysLysLeuPhe 409
 QY 133 CATGACTGCCTCCACCAATATGAAG-----ATCTTTATCTTCTCTTC 177
 Db 410 SerAsnTyrThrSerProAsnProLysAsnSerAsnSerAsnLeuTyr-SerIleSerSe 429
 QY 178 ATTATGGCTCTCATCTAGCCATGATTAGAGCTGATTCATCTGAGAGAAACGTCACAGG 237
 Db 429 lleuSerlleSerSerSerProSerProleuProleuHisSerProAspProValLysG1 449
 QY 238 AAACGGA-----AAAAATCATATAGAGA 261
 Db 449 yAsnSerPheArglleAsnTyrProGluThrProHisLeuTyrLysAsnSerGluThrAs 469
 QY 262 TATTTTC-----AACATACCGCATATCAACGATAT 294
 Db 469 pPheMetThrAsnGlnArgGluGlnLeuAsnHisAsnSerPheAlaHislleAlaPro11 489
 QY 295 CCACTAAATATCTCTCTCGCTATCCATTTCTTAAATGTGCTTAGTAACATACAGAC 354
 Db 489 eAsn-----ThrLysAla11leThrSerProSerArgTh 500
 QY 355 A-----TGATTAGAGAGATTTTTCATCATGATTTTCTCT--ACTCTTTCTGTTGT 402
 Db 500 rAlaThrProLysLeuGlnArg-----PheProGlnThrIleSerMetAs 515
 QY 403 GTTGAAACCATCTTTTCAATAGATATAAACAAGAAAAAATAATCAGTCAAGTACGTGCA 462
 Db 515 nLeu-----AsnMetAsnSerAsnGlyHisSerSerAlaThrSerThrIleG1 531
 QY 463 CAACACATACCTTGGATCAATCAATATCAATATTTTAAACATATAATATGATGCTC 517
 Db 531 nProSerCysLeuSerLeuSer-----AsnAsnAspSerLeu 543

RESULT 12

US-08-286-819A-25
 ; Sequence 25, Application US/08286819A
 ; Patent No. 5871910
 ; GENERAL INFORMATION:
 ; APPLICANT: ARTHUR, MICHEL
 ; APPLICANT: DUKTA-MALEN, SYLVIE
 ; APPLICANT: MOLINAS, CATHERINE
 ; APPLICANT: COURVALIN, PATRICE
 ; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
 ; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
 ; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
 ; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: F.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/286,819A

FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/174,682
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: ORLOH, NO. 5871910man P.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 660-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-286-819A-25

Alignment Scores:		
Pred. No.:	8.32	Length: 161
Score:	66.50	Matches: 21
Percent Similarity:	50.0%	Conservative: 8
Best Local Similarity:	36.21%	Mismatches: 18
Query Match:	6.46%	Indels: 11
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91	TCTAGCAAGAACATCTCCTGAAGCATCAGAATTTTCATCTTTTCATGACTGGACTCCACCA	150
QY		
125	SeRasn-----LysHisMetAsnGlnLysLysLeuAsp-----	135
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151	AATATGAAGAGATCTTTATCTTTGTCTTCATTATGCTCTCATCTCTAGCCATGATT	204
QY		
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RESULT 13

US-08-980-357-25
; Sequence 25, Application US/08980357
; Patent No. 6013508

: GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE

APPLICANT: COORVALIN, FAIRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
EXPRESSION OF RESISTANCE TO GLYCOPETIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-357-25

Alignment Scores:		
Pred. No.:	8.32	Length:
Score:	66.50	Matches:
Percent Similarity:	50.00%	Conservative:
Best Local Similarity:	36.21%	Mismatches:
Query Match:	6.46%	Indels:
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US-10-079-754A-4 (1-604) x US-08-980-357-25 (1-161)

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QY	91	TCTAGCAAAAGAACATCTCCTGAAGCATCAGAATTTTCATCTTCATCATGGAGACTCCACCA	150
Db	125	SerAsn-----LysHisMetAsnGlnLysLeuAsp-----	135
QY	151	AATATGAAGATCTTTATCTTGCTTCTTATTATGGCTCTCATCTCATCCCATGATT	204
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RESULT 14

RESULTS 14
US-09-393-634-60
; Sequence 60, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick

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Run on: August 6, 2004, 17:14:11 ; Search time 48.5 Seconds
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Title: US-10-079-754A-4

Perfect score: 1029

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Dgapop 6.0 , Delcxt 7.0

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 2582470

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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2	316	30.7	58	13	US-10-079-754A-10	Sequence 10, Appli
3	315	30.6	58	13	US-10-079-754A-8	Sequence 8, Appli
4	214.5	20.8	59	13	US-10-079-754A-12	Sequence 12, Appli
5	169	16.4	70	13	US-10-079-754A-9	Sequence 9, Appli
6	112	10.9	21	13	US-10-079-754A-11	Sequence 11, Appli
7	110	10.7	62	12	US-10-210-172-168	Sequence 168, App
8	95	9.2	51	9	US-09-917-340-19	Sequence 19, Appli
9	94.5	9.2	78	10	US-09-992-600A-6	Sequence 6, Appli
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11	94.5	9.2	78	10	US-09-992-095B-6	Sequence 6, Appli
12	94.5	9.2	78	10	US-09-999-570-6	Sequence 6, Appli
13	94.5	9.2	78	14	US-10-000-489-6	Sequence 6, Appli
14	94.5	9.2	78	14	US-10-000-986-6	Sequence 6, Appli
15	94.5	9.2	78	14	US-10-154-678-6	Sequence 6, Appli
16	78	7.6	885	16	US-10-149-310-246	Sequence 246, App
17	77	7.5	1830	12	US-10-424-599-147146	Sequence 147146,
18	76.5	7.4	197	9	US-09-811-284-197	Sequence 197, App
19	75	7.2	423	9	US-09-870-759-103	Sequence 103, App
20	75	7.2	423	10	US-09-751-708A-103	Sequence 103, App
21	74.5	7.2	174	16	US-10-437-963-149428	Sequence 149428, A
22	73.5	7.1	240	12	US-10-282-122A-54218	Sequence 54218, A
23	73.5	7.1	246	16	US-10-389-566-1227	Sequence 1227, Ap
24	73.5	7.1	382	15	US-10-369-493-5291	Sequence 5291, Ap
25	73	7.0	373	13	US-10-114-893-204	Sequence 204, App
26	73	7.1	1680	16	US-10-437-963-192175	Sequence 192175,
27	72.5	7.0	833	16	US-10-437-963-130430	Sequence 130430,
28	72.5	7.0	1428	16	US-10-437-963-193953	Sequence 193953,
29	72.5	7.0	1504	16	US-10-437-963-192104	Sequence 192104,
30	72	7.0	806	12	US-10-282-122A-63502	Sequence 63502, A
31	71	6.9	1201	15	US-10-214-529-7	Sequence 7, Appli
32	70.5	6.9	1363	16	US-10-437-963-192041	Sequence 192041,
33	70	6.8	233	12	US-10-351-334-176	Sequence 176, App
34	70	6.8	276	12	US-10-424-599-154373	Sequence 154373,
35	70	6.8	294	12	US-10-424-599-156848	Sequence 156848,
36	70	6.8	309	12	US-10-510-332-131	Sequence 131, App
37	69.5	6.8	614	12	US-10-282-122A-53563	Sequence 53563, A
38	69	6.7	229	12	US-10-282-122A-71761	Sequence 71761, A
39	69	6.7	317	12	US-10-424-599-159483	Sequence 159483,
40	69	6.7	406	15	US-10-369-493-2232	Sequence 2232, Ap
41	69	6.7	454	12	US-10-282-122A-52793	Sequence 52793, A
42	69	6.7	1517	16	US-10-437-963-127400	Sequence 127400,
43	68.5	6.6	273	9	US-09-939-980-395	Sequence 395, App
44	68	6.6	259	16	US-10-437-963-148811	Sequence 148811,
45	68	6.6	369	12	US-10-335-977-7067	Sequence 7067, Ap

ALIGNMENTS

RESULT 1

US-10-079-754A-7
; Sequence 7, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-7

Alignment Scores:
Pred. No.: 4.13e-29 Length: 58
Score: 316.00 Matches: 58
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 30.71% Indels: 0
DB: 13 Gaps: 0

US-10-079-754A-4 (1-604) x US-10-079-754A-7 (1-58)

QY 154 ATGAAGATCTTTATCTTTGCTTCTCATATGCTCTCATCTACCATGATTAGAGCTGAT 213
DB 1 MetLysIlePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20

QY 214 TCATCTGAAGAGAACGTCACAGGAAACGGAAAAACATCATAGAGGATATTTCAACAA 273
DB 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40

QY 274 TACCAGCCATATCAACGATATCCACTAAATATCTCTCGGTATCCATTCTCT 327
DB 41 TyrGlnProTyrGlnArgTyrProLeuAsnTyrProProAlaTyrProPhePro 58

RESULT 2
US-10-079-754A-10
; Sequence 10, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT FILING DATE: 2002-02-19
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 58
; ORGANISM: Bovine
US-10-079-754A-8

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Best Local Similarity: 98.28% Mismatches: 0
Query Match: 30.61% Indels: 0
DB: 13 Gaps: 0

US-10-079-754A-4 (1-604) x US-10-079-754A-8 (1-58)

QY 154 ATGAAGATCTTTATCTTTGCTTCTCATATGCTCTCATCTACCATGATTAGAGCTGAT 213
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QY 214 TCATCTGAAGAGAACGTCACAGGAAACGGAAAAACATCATAGAGGATATTTCAACAA 273
DB 21 SerSerGluGluLysArgHisArgLysArgLysLysHisArgGlyTyrPheGlnGln 40

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RESULT 4
US-10-079-754A-12
; Sequence 12, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT FILING DATE: 2002-02-19
; CURRENT APPLICATION NUMBER: US/10/079,754A
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; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-12

```

```

Alignment Scores:
Pred. No.: 7,4e-17 Length: 59
Score: 214.50 Matches: 47
Percent Similarity: 78.33% Conservativeness: 0
Best Local Similarity: 78.33% Mismatches: 1
Query Match: 20.85% Indels: 12
DB: 13 Gaps: 1

```

```
US-10-079-754A-4 (1-604) x US-10-079-754A-12 (1-59)
```

```

QY 154 ATGAGATCTTATCTTTGCTTCATTATGCTCTCATCTAGCCATGATTAGAGCTGAT 213
DB 1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
QY 214 TCATCTGAAGAGAAACGTCACAGAAACGGAAAAACATCAT 255
DB 21 SerSerGluGluLysArgHisArgLysArgLysHisHisValAspArgSerProGlu 40
QY 256 -----AGAGATATTTTCAACATATCCAGCCATATCAACGATATCCAC 298
DB 41 PheLeuLeuIleGlnGlu-AspIlePheAsnAsnThrSerHisIleAsnAspIleHis 59

```

```

RESULT 5
US-10-079-754A-9
; Sequence 9, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-9

```

```

Alignment Scores:
Pred. No.: 2.37e-11 Length: 70
Score: 169.00 Matches: 33
Percent Similarity: 100.00% Conservativeness: 1
Best Local Similarity: 97.06% Mismatches: 0

```

```

Query Match: 16.42% Indels: 0
DB: 13 Gaps: 0

```

```
US-10-079-754A-4 (1-604) x US-10-079-754A-9 (1-70)
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```

QY 154 ATGAGATCTTATCTTTGCTTCATTATGCTCTCATCTAGCCATGATTAGAGCTGAT 213
DB 1 MetLysilePheIlePheValPheIleMetAlaLeuIleLeuAlaMetIleArgAlaAsp 20
QY 214 TCATCTGAAGAGAAACGTCACAGAAACGGAAAAACATCAT 255
DB 21 SerSerGluGluLysArgHisArgLysArgLysHisHis 34

```

```
RESULT 6
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```

US-10-079-754A-11
; Sequence 11, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Bovine
US-10-079-754A-11

```

```

Alignment Scores:
Pred. No.: 0.000143 Length: 21
Score: 112.00 Matches: 18
Percent Similarity: 100.00% Conservativeness: 1
Best Local Similarity: 94.74% Mismatches: 0
Query Match: 10.88% Indels: 0
DB: 13 Gaps: 0

```

```
US-10-079-754A-4 (1-604) x US-10-079-754A-11 (1-21)
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```

QY 265 TTTCACATATCCAGCCATATCAACGATATCCACTAAATATCCCTCCGCGTATCCA 321
DB 1 PheGlnGlnTyxGlnProIlyGluArgIlyrProLeuAsnTyxProProAlaIlyrPro 19

```

```
RESULT 7
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```

US-10-210-172-168
; Sequence 168, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie

```

APPLICANT: Voss, Edward
APPLICANT: Boldog, Ferenc
APPLICANT: Gorman, Linda
APPLICANT: Leite, Mario
APPLICANT: Vernet, Corine
APPLICANT: Anderson, David
APPLICANT: Guo, Xiaojia
APPLICANT: Zhong, Mei
APPLICANT: Gezlach, Valerie
APPLICANT: Hjalt, Tord
APPLICANT: Rastelli, Luca
APPLICANT: Spytek, Kimberly
APPLICANT: Edinger, Shlomit
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Alscbrook II, John
APPLICANT: Leplev, Denise et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-416 A
CURRENT APPLICATION NUMBER: US/10/210,172
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 60/310,951
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/313,201
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR FILING DATE: 2001-08-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 327
SOFTWARE: Curaseq1ist version 0.1
SEQ ID NO 168
LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-172-168
Alignment Scores:
Pred. No.: 0.000307 Length: 62
Score: 110.00 Matches: 27
Percent Similarity: 61.82% Conservative: 7
Best Local Similarity: 49.09% Mismatches: 19
Query Match: 10.69% Indels: 2
DB: 12 Gaps: 2
US-10-079-754a-4 (1-604) x US-10-210-172-168 (1-62)
QY 154 ATGAAGATCTTTAATCTTTGTTTCATATGCTCTCATCTAGCCATGATAGAGCTGAT 213
Db 1 MetLysPheLeuValPheAlaPheLeuAlaLeuMetValSerMetIleGlyAlaasp 20
QY 214 TCATCTGAAGAGAACGTCACAGGAAACCGAAAAACATCATAGAGGATATTTTCACAA 273
Db 21 SerSerGluGluLysPheLeuArgArgIleGlyArgPheGlyTyrGlyTyr---GlyPro 39
QY 274 TACAGCCATATCAACGATATCCATAATATCTCTCTGGGTAT 318
Db 40 TyrGlnProValProGluGlnProLeu---TyrProGlnProTyr 53

RESULT 8
US-09-917-340-19
; Sequence 19, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan P.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-08468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-19
Alignment Scores:
Pred. No.: 0.0191 Length: 51
Score: 95.00 Matches: 22
Percent Similarity: 59.57% Conservative: 6
Best Local Similarity: 46.81% Mismatches: 13
Query Match: 9.23% Indels: 6
DB: 9 Gaps: 2
US-10-079-754a-4 (1-604) x US-09-917-340-19 (1-51)
QY 154 ATGAAGATCTTTAATCTTTGTTTCATATGCTCTCATCTAGCCATGATAGAGCTGAT 213
Db 1 MetLysPhePheValPheAlaLeuAlaLeuMetLeuSerMetThrGlyAlaasp 20
QY 214 TCATCTGAAGAGAACGTCAC---AGGAAACGGAAAAACAT-----CAT 255
Db 21 SerHisAlaLysArgHisGlyTyrLysArgLysPheHisGluLysHisHisSerHis 40
QY 256 AGAGGATATTTTCAACAATAC 276
Db 41 ArgGlyTyrArgSerAsnTyr 47
RESULT 9
US-09-992-600A-6
; Sequence 6, Application US/09992600A
; Publication NO. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91 USA.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114


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DB: 14 Gaps: 1
US-10-079-754A-4 (1-604) x US-10-000-986-6 (1-78)

QY 154 ATGAAGATCTTTATCTTTGCTTCATTCATTCCTGCTCTCATCTAGCCATGATTAGAGCTGAT 213
Db 1 MetLysPheValPheAlaLeuValLeuAlaLeuMetIleSerAlaAsp 20
QY 214 TCATCTGAAGAAACGCTCAGGAAACGGAAACACATCATAGAGGATATTTTCAACAA 273
Db 21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis----- 34
QY 274 TACAGGCATATCAACGATATCCACTAAATATCTCTCGGTAT 318
Db 35 ---GluLysHisHisSerTyrHisIleThrLeuLeuProLeuPhe 48

RESULT 15
US-10-154-678-6
; Sequence 6, Application US/10154678
; Publication No: US20030162186A1
; GENERAL INFORMATION:
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 182.US1.REG
; CURRENT APPLICATION NUMBER: US/10/154,678
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 6
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19..-1
US-10-154-678-6

Alignment Scores:
Pred. No.: 0.0238 Length: 78
Score: 94.50 Matches: 18
Percent Similarity: 56.36% Conservative: 13
Best Local Similarity: 32.73% Mismatches: 17
Query Match: 9.18% Indels: 7
DB: 14 Gaps: 1

US-10-079-754A-4 (1-604) x US-10-154-678-6 (1-78)

QY 154 ATGAAGATCTTTATCTTTGCTTCATTCATTCCTGCTCTCATCTAGCCATGATTAGAGCTGAT 213
Db 1 MetLysPheValPheAlaLeuValLeuAlaLeuMetIleSerAlaAsp 20
QY 214 TCATCTGAAGAAACGCTCAGGAAACGGAAACACATCATAGAGGATATTTTCAACAA 273
Db 21 SerHisGluLysArgHisHisGlyTyrArgArgLysPheHis----- 34
QY 274 TACAGGCATATCAACGATATCCACTAAATATCTCTCGGTAT 318
Db 35 ---GluLysHisHisSerTyrHisIleThrLeuLeuProLeuPhe 48
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Search completed: August 6, 2004, 17:24:49
Job time : 49.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2004, 05:31:03 ; Search time 2769 Seconds
(without alignments)
9454.385 Million cell updates/sec

Title: US-10-079-754a-4
Perfect score: 604
Sequence: 1 gaagtatttcagttctata.....tatcaagcataaaaaaaa 604

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_ov:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
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- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
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- 25: em_pl:*
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- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pin:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sv:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	141	23.3	195534	2	AC134173	AC134173 Bos tauru
2	77	12.7	566	9	BC017835	BC017835 Homo sapi
3	77	12.7	3235	9	AK131070	AK131070 Homo sapi
4	75.4	12.5	357	6	BD071675	BD071675 Secreted
5	70.4	11.7	438	6	AX588147	AX588147 Sequence
6	70.4	11.7	438	6	AX588483	AX588483 Sequence
7	70.4	11.7	438	6	AX616321	AX616321 Sequence
8	68.2	11.3	524	9	HUMHIS2X	M26665 Human hist
9	68.2	11.3	558	9	BC009791	BC009791 Homo sapi
10	68.2	11.3	1824	9	AK129614	AK129614 Homo sapi
11	68.2	11.3	2499	9	AK130503	AK130503 Homo sapi
12	68.2	11.3	2537	9	AK130505	AK130505 Homo sapi
13	67.6	11.2	542	9	HUMSTTRNA	M18371 Human stath
14	67.6	11.2	552	9	HUMSTATHA	M18078 Human stath
15	67.6	11.2	1584	6	AX747668	AX747668 Sequence
16	67.6	11.2	1584	9	AK092578	AK092578 Homo sapi
17	67.2	11.1	203	6	BD071749	BD071749 Secreted
18	66.6	11.0	480	9	HUMHIS1X	M26664 Human hist
19	65.6	10.9	486	4	AY154893	AY154893 Bos tauru
20	62.6	10.4	491	9	HUNBHRPA	M18372 Human hist
21	60.8	10.1	516	6	BD071674	BD071674 Secreted
22	60.8	10.1	548	6	AX772840	AX772840 Sequence
23	60.4	10.0	231767	2	AC094531	AC094531 Rattus no
24	60.4	10.0	240446	2	AC131219	AC131219 Rattus no
C 25	60.4	10.0	284590	2	AC106950	AC106950 Rattus no
26	59.2	9.8	7550	9	HUMHIS102	L04132 Human hist
27	59.2	9.8	141568	9	AC063956	AC063956 Homo sapi
28	59.2	9.8	185969	2	AC069037	AC069037 Homo sapi
29	56.6	9.4	143842	2	AC134934	AC134934 Bos tauru
30	56.6	9.4	195334	2	AC134173	AC134173 Bos tauru
31	55.8	9.2	176	6	BD071751	BD071751 Secreted
C 32	55.8	9.2	250050	1	BX248584	BX248584 Blochmann
C 33	55.6	9.2	218675	2	AC015847	AC015847 Homo sapi
34	55	9.1	249943	3	AE014823	AE014823 Plasmodiu
C 35	54.6	9.0	49306	3	AC115606	AC115606 Dictyoste
36	54.4	9.0	253001	3	AE014834	AE014834 Plasmodiu
C 37	54.2	9.0	154071	3	AC115598	AC115598 Dictyoste
38	54.2	9.0	250823	3	AE014821	AE014821 Plasmodiu
C 39	53.6	8.9	13449	6	AX346287	AX346287 Sequence
C 40	53.6	8.9	250022	3	AE014824	AE014824 Plasmodiu
41	52.4	8.7	4500	3	AY392442	AY392442 Dictyoste
C 42	52.4	8.7	82139	3	AC115684	AC115684 Dictyoste
C 43	52	8.6	186934	5	BX004887	BX004887 Zebrafish
C 44	52	8.6	349980	6	AX344567	AX344567 Sequence
C 45	51.8	8.6	254436	3	AE014827	AE014827 Plasmodiu

ALIGNMENTS

RESULT 1
AC134173/c
LOCUS
DEFINITION Bos taurus clone RP42-254113, WORKING DRAFT SEQUENCE, 26 unordered pieces.
AC134173
ACCESSION AC134173.1 GI:23306007
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 195534)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, J., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Burch, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.P., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Eathwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loulsegh, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubacan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 195534)
Worley, K.C.
Direct Submission
Submitted (24-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 195534)
Worley, K.C.
Direct Submission
Submitted (27-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: VUAE
Center clone name: RP42-254113
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 82% of reads
Chemistry: Dye-terminator Big Dye: 18% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 185623 bases at least Q40
Consensus quality: 190257 bases at least Q30
Consensus quality: 192466 bases at least Q20
Estimated insert size: 204493; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers	1..195534
2358:	contig of 2358 bp in length
2359	
2458:	gap of unknown length
2459	
5619:	contig of 3161 bp in length
5620	
5719:	gap of unknown length
5720	
8310:	contig of 2591 bp in length
8311	
8410:	gap of unknown length
8411	
11002:	contig of 2592 bp in length
11003	
11102:	gap of unknown length
11103	
14386:	contig of 3284 bp in length
14387	
14886:	gap of unknown length
14887	
17149:	contig of 2663 bp in length
17150	
17249:	gap of unknown length
17250	
21414:	contig of 4165 bp in length
21415	
21514:	gap of unknown length
21515	
25271:	contig of 3657 bp in length
25272	
30645:	contig of 5374 bp in length
30646	
30745:	gap of unknown length
30746	
36182:	contig of 5437 bp in length
36183	
36282:	gap of unknown length
36283	
41956:	contig of 5674 bp in length
41957	
42056:	gap of unknown length
42057	
48094:	contig of 6038 bp in length
48095	
48194:	gap of unknown length
48195	
53214:	contig of 5020 bp in length
53215	
53314:	gap of unknown length
53315	
5849:	contig of 5535 bp in length
58499:	gap of unknown length
58500	
66144:	contig of 7195 bp in length
66145	
66244:	gap of unknown length
66245	
73033:	contig of 6789 bp in length
73034	
73133:	gap of unknown length
73134	
80030:	contig of 6897 bp in length
80031	
80130:	gap of unknown length
80131	
87761:	contig of 7831 bp in length
87762	
87861:	gap of unknown length
87862	
95726:	contig of 7865 bp in length
95727	
95826:	gap of unknown length
95827	
105054:	contig of 9228 bp in length
105055	
105154:	gap of unknown length
105155	
116716:	contig of 11562 bp in length
116717	
116816:	gap of unknown length
116817	
128293:	contig of 11477 bp in length
128294	
128393:	gap of unknown length
128394	
138140:	contig of 9747 bp in length
138141	
138240:	gap of unknown length
138241	
150687:	contig of 12447 bp in length
150688	
150787:	gap of unknown length
150788	
166414:	contig of 15627 bp in length
166415	
166514:	gap of unknown length
166515	
195534:	contig of 29020 bp in length.

FEATURES

Query Match 23.3%; Score 141; DB 2; Length 195534;
Best Local Similarity 100.0%; Pred. No. 2.3e-17;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAAGTATTTCGTTCTATATATAGATCTCTACTGATGTAATACAAACAAATGAA 60

Db	47365	GAAGTATTTTCAGTCTCTATAAATAGATCTCATAACTGATGTAATTAACAAAACAAATGAA	47306
QY	61	GGATTTCAAGGATTTAAACACACGAGTCTTTCTAGCAAGAACATCTCTGAGCATCAG	120
Db	47305	GGATTTCAAGGATTTAAACACACGAGTCTTTCTAGCAAGAACATCTCTGAGCATCAG	47246
QY	121	AAATTCATCTTTTCATGACTGG	141
Db	47245	AAATTCATCTTTTCATGACTGG	47225
RESULT 2			
LOCUS	BC017835	566 bp	linear PRI 04-OCT-2003
DEFINITION	Homo sapiens histatin 1, mRNA (cdna clone MGC:22502 IMAGE:4289874), complete cds.		
ACCESSION	BC017835		
VERSION	BC017835.1 GI:17389614		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 566)		
1	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheet, T.E., Brownstein, M.J., Ustin, T.B., Leshchiner, I.S., Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
MEDLINE	22388257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 566)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		
Location/Qualifiers	1..566 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:22502 IMAGE:4289874" /tissue_type="Skeletal Muscle" /clone_lib="NIH MGC_81" /lab_host="DH10B" /note="Vector: pDNR-LIB"		
gene	1..566 /gene="HTN1" /note="synonym: HIS1" /db_xref="LocusID:3346" /db_xref="MIM:142701" 68..241 /codon_start=1 /product="histatin 1" /protein_id="AAH17835.1" /db_xref="GI:17389615" /db_xref="LocusID:3346" /translation="MKFEFVALVLMISMISADSHEKHHGYYRKKPEKHSHREFF FYGYGSNLYDN"		
CDS	Query Match 12.7%; Score 77; DB 9; Length 566; Best Local Similarity 59.8%; Pred. No. 7.3e-05; Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1; QY 120 GAATTTTCATCTTTTCATGACTGCTCCACCAATAATGAAGATCTTTATCTTTGCTTTCAT 179 Db 34 GACTCTCTCTTGTAGTAAAGACTCAGCAACTATGAAGTTTTTTGCTTTGCTTTAGT 93 QY 180 TATGCTCTCTCTCTAGCATGATTTAGAGCTGATTCATCTGAGAGAAACGTCACAGGAA 239 Db 94 CTGCTCTCTCTCTAGTTCATGATTTAGCGCTGATTCATGATGAAAGACATCATGGGTA 153 QY 240 ACGGAAAAAATCATGATGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT 299 Db 154 TAGAGAAAAATTCAT-----GAAAAGATCATTCACATCGAGAATTTCCATTTATGG 207 QY 300 AAATATCTCTCTGCTGATTCATTTCTTTAAATGCTCTTAGTAACTACAGGACATCAT 359 Db 208 GGACTATGGATCAAAATATCTATATGACAATGATATCTTAGTAACTATCGGGCATGAT 267 QY 360 TAGAGAGATTT 370 Db 268 TATAGAGGTTT 278		
FEATURES	source AK131070 Homo sapiens cDNA FLJ29036 fis, clone SLV00594. AK131070 Homo sapiens (human) AK131070.1 GI:34528324 cligo capping; fis (full insert sequence). Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiroaka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y.; Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S. NEDO human cDNA sequencing project Unpublished 2 (bases 1 to 3235) Sugano, S. and Suzuki, Y. Direct Submission RESULT 3 AK131070 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 36 Row: a Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21359863.

JOURNAL

Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-Ku, Tokyo 108-8639, Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES

source
1..3235
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SLV00594"
/tissue_type="salivary gland"
/clone_lib="SLV"
/note="cloning vector: pME18SFL3"

ORIGIN

Query Match 12.7%; Score 77; DB 9; Length 3235;
Best Local Similarity 59.8%; Pred. No. 5.5e-05;
Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 120 GAATTTTCATCTTTCATGACCTGGACTCCACCAATATGAGATCTTTATCTTTGCTTCAT 179
DB 2730 GACTCTCTCTTGAGTAAAGGACTCAGCACTATGAGATTTTTCCTTTGCTTTAGT 2789
QY 180 TATGGCTCTCATCTACGCCATGATAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
DB 2790 CTTCGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 2849
QY 240 ACGGAAACACATCATAGAGGATTTTCAACATACAGCCATATCAAGCATATCCACT 299
DB 2950 TAGAAGAAATTCAT-----GAAAGCATATTCATCGAGATTTCCATTTATGG 2903
QY 300 AAATTATCTCTCTCGTCATGATTCATCTTAAATGCTGTAGTAACACAGACATGAT 359
DB 2904 GGACTATGGATCAATATCTATATGACAATTGATATCCTTAGTATATCATGGGGCATGAT 2963
QY 360 TAGAGAGATTT 370
DB 2964 TATAGAGGTTT 2974

RESULT 4
BD071675
LOCUS BD071675 357 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted expressed sequence tags (sESTs).
ACCESSION BD071675
VERSION BD071675.1 GI:22617278
KEYWORDS JP 2001519667-A/485.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 357)
AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D., Treacy,M., Spaulding,V. and Agostino,M.J.
TITLE Secreted expressed sequence tags (sESTs).
JOURNAL Patent: JP 2001519667-A 485 23-OCT-2001;
GENETICS INSTITUTE INC
COMMENT OS Unidentified
PN JP 2001519667-A/485
PD 23-OCT-2001
PF 10-APR-1998 JP 1998543069
PI 10-APR-1997 US 08/838821
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI DAVID MERBERG.
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:

Double:

CC Topology: Linear;
CC Secreted expressed sequence tags (sESTs)
FH Key location/Qualifiers
FT source 1..357
FT /organism="Unidentified".
Location/Qualifiers
1..357
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES

source
1..357
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 12.5%; Score 75.4; DB 6; Length 357;
Best Local Similarity 59.4%; Pred. No. 0.00016;
Matches 149; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 120 GAATTTTCATCTTTCATGACCTGGACTCCACCAATATGAGATCTTTATCTTTGCTTCAT 179
DB 48 GACTCTCTCTTGAGTAAAGGACTCAGCCAACTATGAGATTTTTCCTTTGCTTTAGT 107
QY 180 TATGGCTCTCATCTACGCCATGATAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
DB 108 CTTCGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 167
QY 240 ACGGAAACACATCATAGAGGATTTTCAACATACAGCCATATCAAGCATATCCACT 299
DB 168 TAGAAGAAATTCAT-----GAAAGCATATTCATCGAGATTTCCATTTATGG 221
QY 300 AAATTATCTCTCTCGTCATGATTCATCTTAAATGCTGTAGTAACACAGACATGAT 359
DB 222 GGACTGTGATCAATATCTATATGACAATTGATATCCTTAGTATATCATGGGGCATGAT 281
QY 360 TAGAGAGATTT 370
DB 282 TATAGAGGTTT 292

RESULT 5

AX588147
LOCUS AX588147 438 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 22 from Patent WO02083898.
ACCESSION AX588147
VERSION AX588147.1 GI:27899822
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

REFERENCE 1
AUTHORS Bejanin,S., Tanaka,H., Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.
TITLE Full-length human cdnas encoding potentially secreted proteins
JOURNAL Patent: WO 02083898-A 22 24-OCT-2002;
GENSET (FR)

FEATURES

source
1..438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
84..320
/note="unnamed protein product"
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/protein_id="CAD61372.1"
/db_xref="GI:27899823"
/translation="MKFFVFLVLMISMISADSHKHHGYRRKFKHHSHYHTL
LPLFEESKSNANEKHNYLLYTLCFRLAPSVIT"

CDS

sig_peptide

/note="Von Heijne matrix score 7.64030745849671 seq

polya_signal

ALVLAALMISMISA/DS"

polya_site

421..438

ORIGIN

Query Match 11.7%; Score 70.4; DB 6; Length 438;
Best Local Similarity 69.9%; Pred. No. 0.0013;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTCATCTTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTGTCTTCAT 179
|||
Db 50 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTCTTTTGTCTTTGCTTTAGT 109
|||

QY 180 TATGGCTCTCATCTAGCCATGATTAGCTGATTCATCTGAAGAGAAAACGTCACAGGAA 239
|||
Db 110 CTGGCTCTCATGATTTCCATGATTAGCTGATTCATGATGAAGAGACATCATGGGTA 169
|||

QY 240 ACGGAAAAAATCAT 255
|||
Db 170 TAGAAGAAAATTCAT 185
|||

RESULT 6

AX588483
LOCUS AX588483 438 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 358 from Patent WO02083898.
ACCESSION AX588483
VERSION AX588483.1 GI:27900156
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Homo sapiens
BEJANIN,S., TANAKA,H., DUMAS MILNE EDWARDS,J.B., JOBERT,S. and
GIORDANO,J.Y.
AUTHORS Full-length human cdnas encoding potentially secreted proteins
TITLE Patent: WO 02083898-A 358 24-OCT-2002;
JOURNAL GENSET (FR)
FEATURES Location/Qualifiers
source 1..438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
84..320
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD61539.1"
/db_xref="GI:27300157"
/db_xref="REMITREMBL:CAD61539"
/translation="MKFFVFLVLMISMISADSHEKHHGYRRKFHEKHSHYHITL
LPLFEESKSNANEKHYNLLYTLCLRLAFSIVT"
84..140
/note="Von Heijne matrix score 7.599999990463257 seq
ALVLMISMISA/DS"
sig_peptide

ORIGIN

Query Match 11.7%; Score 70.4; DB 6; Length 438;
Best Local Similarity 69.9%; Pred. No. 0.0013;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTCATCTTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTGTCTTCAT 179
|||
Db 50 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTCTTTTGTCTTTGCTTTAGT 109
|||

QY 180 TATGGCTCTCATCTAGCCATGATTAGCTGATTCATCTGAAGAGAAAACGTCACAGGAA 239
|||
Db 110 CTGGCTCTCATGATTTCCATGATTAGCTGATTCATGATGAAGAGACATCATGGGTA 169
|||

QY 240 ACGGAAAAAATCAT 255
|||
Db 170 TAGAAGAAAATTCAT 185
|||

RESULT 7

AX616321

ORIGIN

AX616321
LOCUS AX616321 438 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 5 from Patent WO02094864.
ACCESSION AX616321
VERSION AX616321.1 GI:28447365
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
SOURCE Homo sapiens
BEJANIN,S. and TANAKA,H.
AUTHORS Human cdnas and proteins and uses thereof
TITLE Patent: WO 02094864-A 5 28-NOV-2002;
JOURNAL GENSET (FR)
FEATURES Location/Qualifiers
source 1..438
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1..83
84..320
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD67625.1"
/db_xref="GI:28447366"
/db_xref="REMITREMBL:CAD67625"
/translation="MKFFVFLVLMISMISADSHEKHHGYRRKFHEKHSHYHITL
LPLFEESKSNANEKHYNLLYTLCLRLAFSIVT"
3'UTR 318..438
polyA_signal 397..402
polyA_site 423..438
ORIGIN

Query Match

11.7%; Score 70.4; DB 6; Length 438;
Best Local Similarity 69.9%; Pred. No. 0.0013;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTCATCTTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTGTCTTCAT 179
|||
Db 50 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTCTTTTGTCTTTGCTTTAGT 109
|||

QY 180 TATGGCTCTCATCTAGCCATGATTAGCTGATTCATCTGAAGAGAAAACGTCACAGGAA 239
|||
Db 110 CTGGCTCTCATGATTTCCATGATTAGCTGATTCATGATGAAGAGACATCATGGGTA 169
|||

QY 240 ACGGAAAAAATCAT 255
|||
Db 170 TAGAAGAAAATTCAT 185
|||

RESULT 8

HUMHIS2X
LOCUS HUMHIS2X 524 bp mRNA linear PRI 31-DEC-1994
DEFINITION Human histatin 2 (HIS2) mRNA, complete cds.
ACCESSION M26665
VERSION M26665.1 GI:292145
KEYWORDS histatin 2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
EUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;
MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
REFERENCE 1 (bases 1 to 524)
AUTHORS Sabatini,L.M. and Azen,E.A.
TITLE Histatins, a family of salivary histidine-rich proteins, are
encoded by at least two loci (HIS1 and HIS2)
JOURNAL Biochem. Biophys. Res. Commun. 160 (2), 495-502 (1989)
MEDLINE 89246491
PubMed 2719677
COMMENT Original source text: Homo sapiens parotid gland cDNA to mRNA.
FEATURES Location/Qualifiers
source 1..524
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
 /tissue_type="parotid gland"
 1. .524
 /gene="HIS2"
 72. .227
 /gene="HIS2"
 /codon_start=1
 /product="histatin 2"
 /protein_id="AA58646.1"
 /db_xref="GI:292146"
 /translation="MKFFVFLILALMLSGADSHAKRHGHYKRFHEKHHSHRGYR
 SNLYDN"
 polyA_signal
 506. .511
 /gene="HIS2"

ORIGIN

Query Match 11.3%; Score 68.2; DB 9; Length 524;
 Best Local Similarity 65.4%; Pred. No. 0.0034;
 Matches 100; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 120 GAATTTTCATCTTTTCATGACGTCACCAAAATATGAAGATCTTTATCTTTGCTTTTCAT 179
 Db 38 GATTCCTCTTTGAGTAAAGGACTGAGCACTATGAAGTTTTTTTGTTCCTTAAT 97
 QY 180 TATGGCTCTCATCTGACCATGATAGAGTGATTCATCTGAAGAAACGTCACAGGAA 239
 Db 98 CTGGCTCTCATGCTTTCCATGACTGGAGCTGATTCACATGCAAGAGACATCATGGTA 157
 QY 240 ACGGAAACATCATAGAGGATATTTCAACA 272
 Db 158 TAAAGAAATTCATGAAAGCATCTTCA 190

RESULT 9

BC009791 Homo sapiens histatin 3, mRNA (CDNA clone MGC:13578 IMAGE:4293405),
 LOCUS complete cds.
 ACCESSION BC009791
 VERSION BC009791.1 GI:14602560
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 558)
 Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
 Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 22388257
 PUBLISHED 12477932
 REFERENCE 2 (bases 1 to 558)
 Srausberg, R.
 Direct Submission
 TITLE Submitted (02-JUL-2001) National Institutes of Health, Mammalian

REMARK
COMMENT

Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansys@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IMAGE Plate: 19 Row: 0 Column: 1
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4557652.

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gene

CDS

ORIGIN

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 Matches 100; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 120 GAATTTTCATCTTTTCATGACGTCACCAAAATATGAAGATCTTTATCTTTGCTTTTCAT 179
 Db 42 GATTCCTCTTTGAGTAAAGGACTGAGCACTATGAAGTTTTTTTGTTCCTTAAT 101
 QY 180 TATGGCTCTCATCTGACCATGATAGAGTGATTCATCTGAAGAAACGTCACAGGAA 239
 Db 102 CTGGCTCTCATGCTTTCCATGACTGGAGCTGATTCACATGCAAGAGACATCATGGTA 161
 QY 240 ACGGAAACATCATAGAGGATATTTCAACA 272
 Db 162 TAAAGAAATTCATGAAAGCATCTTCA 194
 RESULT 10
 AK129614
 LOCUS Homo sapiens CDNA FLJ26103 fis, clone SLV07780.
 DEFINITION AK129614
 ACCESSION AK129614.1 GI:34526191
 VERSION AK129614.1
 KEYWORDS cligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fldnna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
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ORIGIN
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Best Local Similarity 65.4%; Pred. No. 0.0028;
Matches 100; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
Qy 120 GAATTTTCATCTTCATGCTGCATCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
Db 1338 GATTCTCTCTTGTAGTAAAGGACTCAGCCAACTATGAAGTTTGTGTTGCTTTAAT 1397
Qy 180 TATGGCTCTATCTGCTAGCTGATTCATCTGAGAGAAAGCTCAGAGAA 239
Db 1398 CTGGCTCTCATGCTTTCCATGATCTGGAGCTGATTCATCCAAAGAGATCATGGTA 1457
Qy 240 ACGGAAAAACATCATGAGGATATTTTCAACA 272
Db 1458 TAAAGAAATTCATGAGGATATTTTCAACA 1490
RESULT 11
AK130503 2499 bp mRNA linear PRI 10-SEP-2003
LOCUS Homo sapiens cDNA FLJ26993 fis, clone SLV03847, highly similar to Histatin 3 precursor.
DEFINITION AK130503
ACCESSION AK130503
VERSION AK130503.1 GI:34527320
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2499)
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fldnna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.
FEATURES
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Qy 120 GAATTTTCATCTTCATGCTGCATCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
Db 2013 GATTCTCTCTTGTAGTAAAGGACTCAGCCAACTATGAAGTTTGTGTTGCTTTAAT 2072
Qy 180 TATGGCTCTATCTGCTAGCTGATTCATCTGAGAGAAAGCTCAGAGAA 239
Db 2073 CTGGCTCTCATGCTTTCCATGATCTGGAGCTGATTCATCCAAAGAGATCATGGTA 2132
Qy 240 ACGGAAAAACATCATGAGGATATTTTCAACA 272
Db 2133 TAAAGAAATTCATGAGGATATTTTCAACA 2165
RESULT 12
AK130505 2537 bp mRNA linear PRI 10-SEP-2003
LOCUS Homo sapiens cDNA FLJ26995 fis, clone SLV04017, highly similar to Histatin 3 (HIN3).
DEFINITION AK130505
ACCESSION AK130505
VERSION AK130505.1 GI:34527322
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2537)
AUTHORS Sugano, S. and Suzuki, Y.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: fldnna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.

FEATURES

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ORIGIN

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Best Local Similarity 65.4%; Pred. No. 0.0026;
Matches 100; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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DB 2051 GATTCCTCTTGAGTAAAGACTCAGCCAACTATGAAATTTTGTCTTTAT 2110
QY 180 TATGGCTCTCATCTCCTAGCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCAAGGAA 239
DB 2111 CTGGCTCTCATGCTTCCATGACTGGAGCTGATTCATGCAAGAGACATCATGGTA 2170
QY 240 ACGGAAACATCATAGAGGATTTTCAACA 272
DB 2171 TAAAGAAATTCATGAAAGCATCATTCACA 2203

RESULT 13

HUMSTTRNA HUMSTTRNA 542 bp mRNA linear PRI 13-JAN-1995
LOCUS Human statherin mRNA, complete cds.
DEFINITION M18371 GI:338610
VERSION statherin.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS Dickinson,D.P., Ridall,A.L. and Levine,M.J.
TITLE Human submandibular gland statherin and basic histidine-rich peptide are encoded by highly abundant mRNA's derived from a common ancestral sequence
JOURNAL Biochem. Biophys. Res. Commun. 149 (2), 784-790 (1987)
MEDLINE 88106506
PUBMED 3426601
COMMENT Original source text: Human female submandibular gland, cDNA to mRNA, clone pBRHSMF98.2.
Draft entry and computer readable copy of sequence [1] kindly provided by D.P.Dickinson 21-MAR-1988.

FEATURES

source
1..542
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/db_xref="taxon:9606"
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1..542
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57..245
/note="statherin precursor"
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gene

CDS

sig_peptide
278 bp upstream of PstI site; chromosome 4q11-q13.

sig_peptide
57..113
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114..242
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/product="statherin"
ORIGIN 262 bp upstream of PstI site; chromosome 4q11-q13.
Query Match 11.2%; Score 67.6; DB 9; Length 542;
Best Local Similarity 61.2%; Pred. No. 0.0044;
Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;
QY 140 GGACTCCACCAATATGAAGATCTTTATCTTGTCTTCATTCATTCCTCCTAGCCCA 199
DB 43 GAACCCAGCCCAACTATGAAGTTCTTGTCTTGTCTTCATCTTGGCTCTCATGGTTCCA 102
QY 200 TCATTAGAGCTGATTCATCTGAAGAGAAACGTCAAGAGAAACGAAACAAACATCATAGAG 259
DB 103 TGAATGGAGCTGATTCATCTGAAGAGAAATTTTCCGTAGAAATTTGGAAGATTCGGTTATG 162
QY 260 GATA-----TTTTCACAAATACCAAGCCATATCAACGATATCCACTAAATATCTCCTCG 313
DB 163 GGTATGGCCCTTATCAGCCAGTTCAGAGAACCACTATATCCACACCACTACCAACAC 222
QY 314 CGT---ATCCATTTCTTAAATATGCTGCTTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 370
DB 223 AATACCAACAATATACCTTTTAAATATCATCATCACTAGTAAGTAAGTAAGTAAGTAAGTAAG 282
RESULT 14
HUMSTATHA HUMSTATHA 552 bp mRNA linear PRI 13-JAN-1995
LOCUS Human statherin mRNA, complete cds.
DEFINITION M18078 GI:338507
VERSION regulatory protein; statherin.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Sabatini,L.M., Carlock,L.R., Johnson,G.W. and Azen,E.A.
TITLE cDNA cloning and chromosomal localization (4q11-13) of a gene for statherin, a regulator of calcium in saliva
JOURNAL Am. J. Hum. Genet. 41 (6), 1048-1060 (1987)
MEDLINE 88074310
PUBMED 3502720
COMMENT Original source text: Human parotid gland, cDNA to mRNA, clone H772B.
Draft entry and computer-readable sequence [1] kindly submitted by L.Sabatini 19-JAN-1988.

FEATURES

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73..129
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/note="statherin signal peptide"
278 bp upstream of PstI site; chromosome 4q11-q13.

Query Match 11.2%; Score 67.6; DB 9; Length 552;
Best Local Similarity 61.2%; Pred. No. 0.0044;
Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;

QY 140 GGACTCCACCAATATGAGATCTTTATCTTTGCTTCATTATGCTCTCATCTAGCCCA 199
DB 59 GAACCCAGCCAACTATGAAGTCTCTTTGCTTCATCTTGGCTCTCATGGTTTCCA 118
QY 200 TGATTAGAGCTGATTCATCTGAGAGAAAGCTCACAGGAACGGAAACATCATAGAG 259
DB 119 TGATTGGAGCTGATTCATCTGAGAGAAATTTTTCGTAGAAATTGGAAGATTTCGGTTATG 178
QY 260 GATA-----TTTCAACAATACCAGCATATCAACGATATCCACTAAATATCTCTCTG 313
DB 179 GGTATGGCCCTTATCAGCCAGTTCAGAACACACACTATACCCACACCATACCAACCAC 238
QY 314 CGT---ATCCATTTCCCTTAAATGCTCTTAGTAACTACAGGACATGATTAGAGATTT 370
DB 239 AATACCAACAATATACCTTTTAAATATCATCATGAAGTAACTGCAGGACATGATTATTGAGGCTT 298

RESULT 15
AX747668 1584 bp mRNA linear PAT 20-JUN-2003
LOCUS AX747668
DEFINITION Sequence 1193 from Patent EP1308459.
ACCESSION AX747668
VERSION AX747668.1 GI:32132056
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuho, Y.
Full-length cDNA sequences
Patent: EP 1308459-A 1193 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
FEATURES
source
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/organism="Homo sapiens"
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ORIGIN

Query Match 11.2%; Score 67.6; DB 6; Length 1584;
Best Local Similarity 61.2%; Pred. No. 0.0037;
Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;

QY 140 GGACTCCACCAATATGAGATCTTTATCTTTGCTTCATTATGCTCTCATCTAGCCCA 199
DB 1083 GAACCCAGCCAACTATGAAGTCTCTTTGCTTCATCTTGGCTCTCATGGTTTCCA 1142
QY 200 TGATTAGAGCTGATTCATCTGAGAGAAAGCTCACAGGAACGGAAACATCATAGAG 259
DB 1143 TGATTGGAGCTGATTCATCTGAGAGAAATTTTTCGTAGAAATTGGAAGATTTCGGTTATG 1202
QY 260 GATA-----TTTCAACAATACCAGCATATCAACGATATCCACTAAATATCTCTCTG 313
DB 1203 GGTATGGCCCTTATCAGCCAGTTCAGAACACACACTATACCCACACCATACCAACCAC 1262
QY 314 CGT---ATCCATTTCCCTTAAATGCTCTTAGTAACTACAGGACATGATTAGAGATTT 370
DB 1263 AATACCAACAATATACCTTTTAAATATCATCATGAAGTAACTGCAGGACATGATTATTGAGGCTT 1322

Search completed: August 15, 2004, 22:31:24
Job time : 2774 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2004, 05:08:11 ; Search time 352 Seconds

(without alignments)
7289.522 Million cell updates/sec

Title: US-10-079-754A-4

Perfect score: 604

Sequence: 1 gaagatttcctgctctata.....tatcaagcataaaaaaaaaa 604

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002s.*

7: Geneseq2003as.*

8: Geneseq2003bs.*

9: Geneseq2003cs.*

10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	604	100.0	604	7 ABX11391	Abx11391 Bovine hi
2	465.4	77.1	505	7 ABX11388	Abx11388 Bovine hi
3	448.2	74.2	585	7 ABX11389	Abx11389 Bovine hi
4	423.4	70.1	525	7 ABX11393	Abx11393 Bovine hi
5	238.4	39.5	267	7 ABX11394	Abx11394 Bovine ma
6	115	19.0	869	7 ABX11390	Abx11390 Bovine hi
7	87	14.4	96	7 ABX11392	Abx11392 Bovine hi
8	75.4	12.5	357	2 AAV89526	AAV89526 EST clone
9	70.4	11.7	438	7 ACC51062	Acc51062 Human Chi
10	70.4	11.7	438	7 ABZ36590	Abz36590 Human GEN
11	70.4	11.7	438	7 ABZ36425	Abz36425 Human GEN
12	68.2	11.3	857	4 AAH98658	AAH98658 Human EST
13	67.6	11.2	552	3 AAA48964	AAA48964 Human sta
14	67.6	11.2	678	9 ADE40261	Ade40261 Human NOV
15	67.6	11.2	1584	9 ADB63039	ADB63039 Human CDN
16	67.2	11.1	203	2 AAV89600	AAV89600 EST clone
17	62.6	10.4	491	3 AAA48965	AAA48965 Human bas
18	62	10.3	406	9 ADE09636	Ade09636 Novel DNA
19	60.8	10.1	417	9 ADE07409	Ade07409 Novel cod
20	60.8	10.1	516	2 AAV89525	AAV89525 EST clone
21	60.8	10.1	548	8 AAL60905	AAL60905 Human sal
22	59.6	9.9	732	8 AAL61238	AAL61238 Human sec
23	58	9.6	457	6 ABQ99552	ABQ99552 Human cod

ALIGNMENTS

RESULT 1

ABX11391

ID ABX11391 standard; cDNA; 604 BP.

XX AC ABX11391;

XX DT 01-MAY-2003 (first entry)

XX DE Bovine histatin like polypeptide, #4, cDNA.

XX KW Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity;

XX KW non-immune defence system; oral candidosis; gene therapy;

XX KW microbial infection; fungal infection; dental caries; plaque; tartar;

XX KW cystic fibrosis; systemic infection; Candida infection; mastitis;

XX KW fungicide; antibacterial.

XX OS Bos taurus.

XX FH Key

XX CDS

XX FT

XX FT

XX FT

XX PN

XX XX

XX PD

XX XX

XX PF

XX PF

XX XX

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

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XX PR

XX PR

XX PR

Claim 1; Page 12; 17pp; English.

The invention discloses isolated histatin polynucleotides and polypeptides, which comprise sequences expressed in bovine. Histatins are histidine rich and specific to the salivary secretions. They are believed to function as part of the non-immune defence system, particularly in the oral cavity and have promise as therapeutic agents in humans with oral candidosis. Also disclosed are compositions comprising the histatin polypeptide or polynucleotide, and at least one component consisting of physiological or pharmaceutical carriers or immunostimulants. The histatin polynucleotide, polypeptide, or the cosmetic composition comprising the polypeptide, is useful for treating (e.g. gene therapy) a disorder in a mammal, particularly microbial or fungal infections. The histatin polynucleotide is also useful in genome mapping, physical mapping or in the positional cloning of genes. Specifically, the polypeptide or polynucleotide is useful for treating fungal or bacterial infections of the oral cavity (e.g. dental caries, plaque or tartar), vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis caused by *Pseudomonas aeruginosa*), mucosa or eye, as well as for treating systemic infections such as systemic candida infection. The polypeptide or polynucleotide is also useful for veterinary applications e.g. for treating mastitis. The sequence presented is a cDNA encoding a bovine histatin like polypeptide

Sequence 604 BP; 222 A; 112 C; 79 G; 191 T; 0 U; 0 Other;

Query Match	100.0%;	Score 604;	DB 7;	Length 604;
Best Local Similarity	100.0%;	Pred. No. 5.2e-120;		
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Db	1	GAAGTATTTTCAGTTCTATATAGATCTCATACACTGATGTAATACAAAACAAATGAA	60	
Qy	61	GGATTTCAAGTATTTAAACACAGCAGTTTCTAGCAAGAAACATCTCTGAAGCATCAG	120	
Db	61	GGATTTCAAGTATTTAAACACAGCAGTTTCTAGCAAGAAACATCTCTGAAGCATCAG	120	
Qy	121	AATTTTCATCTTTCATGACTGAGTCCACCAAAATGAAGATCTTTATCTTTGCTTCATT	180	
Db	121	AATTTTCATCTTTCATGACTGAGTCCACCAAAATGAAGATCTTTATCTTTGCTTCATT	180	
Qy	181	ATGGCTCTCATCTCCAGGCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA	240	
Db	181	ATGGCTCTCATCTCCAGGCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA	240	
Qy	241	CGGAAAAACATCATAGAGGATATTTTCACAAATACCGCCATCAACGATATCCACTA	300	
Db	241	CGGAAAAACATCATAGAGGATATTTTCACAAATACCGCCATCAACGATATCCACTA	300	
Qy	301	AATTTATCTCTCGGTATCCATTTCTTAAATGCTGCTTAGTAACCTACAGGACATGATT	360	
Db	301	AATTTATCTCTCGGTATCCATTTCTTAAATGCTGCTTAGTAACCTACAGGACATGATT	360	
Qy	361	AGAGAGATTTTCAATGATTTTCTACTCTTCTGTTGTTGAAACCATCTTTCA	420	
Db	361	AGAGAGATTTTCAATGATTTTCTACTCTTCTGTTGTTGAAACCATCTTTCA	420	
Qy	421	AATCAATAAACAAAGAAAAAATAATCAGTCAAGTAGTTGCACAAACATATCTGGAATC	480	
Db	421	AATCAATAAACAAAGAAAAAATAATCAGTCAAGTAGTTGCACAAACATATCTGGAATC	480	
Qy	481	AAATATCAATATTTAAAAACATAATATGATGCTCTGACATATGTAATGTTTCTTAC	540	
Db	481	AAATATCAATATTTAAAAACATAATATGATGCTCTGACATATGTAATGTTTCTTAC	540	
Qy	541	TTTCTTTTCTCTGCTCACTTACCATGCTTAAATTAATGATCTTCAAGCATATAAAAA	600	
Db	541	TTTCTTTTCTCTGCTCACTTACCATGCTTAAATTAATGATCTTCAAGCATATAAAAA	600	
Qy	601	AAAA 604		
Db	601	AAAA 604		

RESULT 2
ABX11388
ID ABX11388 standard; cDNA; 505 BP.
XX AC ABX11388;
XX DT 01-MAY-2003 (first entry)
XX DE Bovine histatin like polypeptide, #1, cDNA.
XX KW Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity;
KW non-immun defence system; oral candidosis; gene therapy;
KW microbial infection; fungal infection; dental caries; plaque; tartar;
KW cystic fibrosis; systemic infection; Candida infection; mastitis;
KW fungicide; antibacterial.
XX OS Bos taurus.
XX FH Key Location/Qualifiers
FT CDS 44..220
FT /*tag= a
FT /product= "Histatin like polypeptide"
XX PN US2002164625-A1.
XX PD 07-NOV-2002.
XX PF 19-FEB-2002; 2002US-00079754.
XX PR 23-AUG-1999; 99US-0150330P.
PR 29-OCT-1999; 99US-0162701P.
PR 22-AUG-2000; 2000US-00644190.
PR 27-OCT-2000; 2000US-00699146.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Glenn M, Grigor MR, Molenaar AJ, Davis SR;
WPI: 2003-275306/27.
P-PSDB; ABG75791.
XX New histatin polynucleotides and polypeptides expressed in bovine
tissues, useful for treating bacterial or fungal infections in mammals,
e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
systemic infections.
XX Claim 1; Page 11; 17pp; English.
XX The invention discloses isolated histatin polynucleotides and
polypeptides, which comprise sequences expressed in bovine. Histatins are
histidine rich and specific to the salivary secretions. They are believed
to function as part of the non-immune defence system, particularly in the
oral cavity and have promise as therapeutic agents in humans with oral
candidosis. Also disclosed are compositions comprising the histatin
polypeptide or polynucleotide, and at least one component consisting of
physiological or pharmaceutical carriers or immunostimulants. The
histatin polynucleotide is also useful in genome mapping, physical
mapping or in the positional cloning of genes. Specifically, the
polypeptide or polynucleotide is useful for treating fungal or bacterial
infections of the oral cavity (e.g. dental caries, plaque or tartar),
vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis
caused by *Pseudomonas aeruginosa*), mucosa or eye, as well as for treating
systemic infections such as systemic candida infection. The polypeptide
or polynucleotide is also useful for veterinary applications e.g. for
treating mastitis. The sequence presented is a cDNA encoding a bovine
histatin like polypeptide
XX Sequence 505 BP; 188 A; 96 C; 67 G; 154 T; 0 U; 0 Other;

Glenn M, Grigor MB, Molenaar AJ, Davis SR;
WPI; 2003-275306/27.
P-PSDB; ABG75792.

New histatin polynucleotides and polypeptides expressed in bovine
tissues, useful for treating bacterial or fungal infections in mammals,
e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
systemic infections.

Claim 1; Page 11; 17pp; English.

The invention discloses isolated histatin polynucleotides and
polypeptides, which comprise sequences expressed in bovine. Histatins are
histidine rich and specific to the salivary secretions. They are believed
to function as part of the non-immune defence system, particularly in the
oral cavity and have promise as therapeutic agents in humans with oral
candidosis. Also disclosed are compositions comprising the histatin
polypeptide or polynucleotide, and at least one component consisting of
physiological or pharmaceutical carriers or immunostimulants. The
histatin polynucleotide, polypeptide, or the cosmetic composition
comprising the polypeptide, is useful for treating (e.g. gene therapy) a
disorder in a mammal, particularly microbial or fungal infections. The
histatin polynucleotide is also useful in genome mapping, physical
mapping or in the positional cloning of genes. Specifically, the
polypeptide or polynucleotide is useful for treating fungal or bacterial
infections of the oral cavity (e.g. dental caries, plaque or tartar),
vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis
caused by *Pseudomonas aeruginosa*), mucosa or eye, as well as for treating
systemic infections such as systemic *Candida* infection. The polypeptide
or polynucleotide is also useful for veterinary applications e.g. for
treating mastitis. The sequence presented is a cDNA encoding a bovine
histatin like polypeptide

Sequence 585 BP; 215 A; 111 C; 85 G; 174 T; 0 U; 0 Other;

	Best Local Similarity	99.38;	pred. No. 1.2e-86;		Mismatches	3;	Indels	0;	Gaps	0;
	Marches	450;	Conservative	0;						
QY	138	CTGAC	TCCACCAAAATATGAAGATCTTTATCTTTGTCTTCA	TATGGCTCTCATCCTAGC	197					
Db	133	CAGACT	CCACCAATATGAAGATCTTTATCTTTATCTCA	TATGGCTCTCATCCTAGC	192					
QY	198	CATGAT	TAGAGCTGATTTCACTGAAGAGAAACGTCACAGGAAACGGA	AAAAACATCATAG	257					
Db	193	CATGAT	TAGAGCTGATTTCACTGAAGAGAAACGTCACAGGAAACGGA	AAAAACATCATAG	252					
QY	258	AGGATAT	TTTCAACAATACACAGCGAATATCAACGATATCCACTAAAT	TATCTCTCGCGTA	317					
Db	253	AGGATAT	TTTCAACAATACACAGCGAATATCAACGATATCCACTAAAT	TATCTCTCGCGTA	312					
QY	318	TCCAT	TTTCCCTTAAATGCTGCTAGTAACACAGACATGATAGAGAGATTTT	TTCACAA	377					
Db	313	TCCAT	TTTCCCTTAAATGCTGCTAGTAACACAGACATGATAGAGAGATTTT	TTCACAA	372					
QY	378	TGAT	TTTTTCCCTACTCTTTCTGTTGTTGTA	AAAAACAATGAATAAAAACAAGA	437					
Db	373	TGAT	TTTTTCCCTACTCTTTCTGTTGTTGTA	AAAAACAATGAATAAAAACAAGA	432					
QY	438	AAAAA	AAATCAGTCACGTAGTTGCACACACATCTTGGATCAAA	TATCAATATTTTAA	497					
Db	433	AAAAA	AAATCAGTCACGTAGTTGCACACACATCTTGGATCAAA	TATCAATATTTTAA	492					
QY	498	AACATA	TAATGATAGTCTCGAACTATGTAATTTGGTTTCTACTTTTCT	CTGTGTCAC	557					
Db	493	AACATA	TAATGATAGTCTCGAACTATGTAATTTGGTTTCTACTTTTCT	CTGTGTCAC	552					
QY	558	TTACAT	GCATGCTTAATAAATTCATCTATCAA	590						
Db	553	TTACAT	GCATGCTTAATAAATTCATCTATCAA	585						

XX WPI; 2003-275306/27.
XX New histatin polynucleotides and polypeptides expressed in bovine
PT tissues, useful for treating bacterial or fungal infections in mammals,
PT e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
PT systemic infections.
XX
XX Example 2; Page 15; 17pp; English.
XX
XX The invention discloses isolated histatin polynucleotides and
CC polypeptides, which comprise sequences expressed in bovine. Histatins are
CC histidine rich and specific to the salivary secretions. They are believed
CC to function as part of the non-immune defence system, particularly in the
CC oral cavity and have promise as therapeutic agents in humans with oral
CC candidosis. Also disclosed are compositions comprising the histatin
CC polypeptide or polynucleotide, and at least one component consisting of
CC physiological or pharmaceutical carriers or immunostimulants. The
CC histatin polynucleotide, polypeptide, or the cosmetic composition
CC comprising the polypeptide, is useful for treating (e.g. gene therapy) a
CC disorder in a mammal, particularly microbial or fungal infections. The
CC histatin polynucleotide is also useful in genome mapping, physical
CC mapping or in the positional cloning of genes. Specifically, the
CC polypeptide or polynucleotide is useful for treating fungal or bacterial
CC infections of the oral cavity (e.g. dental caries, plaque or tartar),
CC vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis,
CC caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating
CC systemic infections such as systemic Candida infection. The polypeptide
CC or polynucleotide is also useful for veterinary applications e.g. for
CC treating mastitis. The sequence presented is the bovine mammary tissue
CC cDNA clone which was used to illustrate mRNA expression levels of mammary
CC gland specific sequences
XX
XX Sequence 267 BP; 89 A; 59 C; 43 G; 76 T; 0 U; 0 Other;
SQ
Query Match 39.5%; Score 238.4; DB 7; Length 267;
Best Local Similarity 99.6%; Pred. No. 8.9e-42;
Matches 239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 CTGACTCCACCAATATGAGATCTTATCTTGTCTTCATATGCTCTCATCTAGC 197
Db 28 CAGGACTCCACCAATATGAGATCTTATCTTGTCTTCATATGCTCTCATCTAGC 87
QY 198 CATGATTAGAGCTGATTTCATCTGAAGAGAAACGTCACAGGAACGGAAAAACATCATAG 257
Db 88 CATGATTAGAGCTGATTTCATCTGAAGAGAAACGTCACAGGAACGGAAAAACATCATAG 147
QY 258 AGGATATTTTCAACAATACAGGCAATATCAACGATATCCACTAAATATCTCTCGGTA 317
Db 148 AGGATATTTTCAACAATACAGGCAATATCAACGATATCCACTAAATATCTCTCGGTA 207
QY 318 TCCATTTTCTTAAATGCTGCTTAGTAACACAGGACATGATTAGAGAGATTTTTCACAA 377
Db 208 TCCATTTTCTTAAATGCTGCTTAGTAACACAGGACATGATTAGAGAGATTTTTCACAA 267
RESULT 6
ABX11390
ID ABX11390 standard; cDNA; 869 BP.
XX
XX ABX11390;
AC
XX
XX 01-MAY-2003 (first entry)
DT
XX
XX Bovine histatin like polypeptide, #3, cDNA.
XX
XX Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity;
XX non-immune defence system; oral candidosis; gene therapy;
XX microbial infection; fungal infection; dental caries; plaque; tartar;
XX cystic fibrosis; systemic infection; Candida infection; mastitis;
XX fungicide; antibacterial.
XX
XX Bos taurus.
OS

XX Key Location/Qualifiers
FH CDS 72..284
FT /*tag= a
FT /product= "Histatin like polypeptide"
XX
XX US2002164625-A1.
XX
XX 07-NOV-2002.
XX
XX 19-FEB-2002; 2002US-00079754.
XX
XX 23-AUG-1999; 99US-0150330P.
XX 29-OCT-1999; 99US-016270DP.
XX 22-AUG-2000; 2000US-00644190.
XX 27-OCT-2000; 2000US-00699146.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Glenn M, Grigor MR, Molenaar AJ, Davis SR;
PI WPI; 2003-275306/27.
XX P-PSDB; ABG75793.
XX
XX New histatin polynucleotides and polypeptides expressed in bovine
PT tissues, useful for treating bacterial or fungal infections in mammals,
PT e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
PT systemic infections.
XX
XX Claim 1; Page 12; 17pp; English.
XX
XX The invention discloses isolated histatin polynucleotides and
CC polypeptides, which comprise sequences expressed in bovine. Histatins are
CC histidine rich and specific to the salivary secretions. They are believed
CC to function as part of the non-immune defence system, particularly in the
CC oral cavity and have promise as therapeutic agents in humans with oral
CC candidosis. Also disclosed are compositions comprising the histatin
CC polypeptide or polynucleotide, and at least one component consisting of
CC physiological or pharmaceutical carriers or immunostimulants. The
CC histatin polynucleotide, polypeptide, or the cosmetic composition
CC comprising the polypeptide, is useful for treating (e.g. gene therapy) a
CC disorder in a mammal, particularly microbial or fungal infections. The
CC histatin polynucleotide is also useful in genome mapping, physical
CC mapping or in the positional cloning of genes. Specifically, the
CC polypeptide or polynucleotide is useful for treating fungal or bacterial
CC infections of the oral cavity (e.g. dental caries, plaque or tartar),
CC vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis,
CC caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating
CC systemic infections such as systemic Candida infection. The polypeptide
CC or polynucleotide is also useful for veterinary applications e.g. for
CC treating mastitis. The sequence presented is a cDNA encoding a bovine
CC histatin like polypeptide
XX
XX Sequence 869 BP; 282 A; 157 C; 147 G; 283 T; 0 U; 0 Other;
SQ
Query Match 19.0%; Score 115; DB 7; Length 869;
Best Local Similarity 92.4%; Pred. No. 2.9e-15;
Matches 121; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 138 CTGACTCCACCAATATGAGATCTTATCTTGTCTTCATATGCTCTCATCTAGC 197
Db 56 CAGGACTCCACCAATATGAGATCTTATCTTGTCTTCATATGCTCTCATCTAGC 115
QY 198 CATGATTAGAGCTGATTTCATCTGAAGAGAAACGTCACAGGAACGGAAAAACATCATAG 257
Db 116 CATGATTAGAGCTGATTTCATCTGAAGAGAAACGTCACAGGAACGGAAAAACATCATGT 175
QY 258 AGGATATTTTTC 268
Db 176 ATGATTCTCTC 186
XX
XX RESULT 7

ABX11392
ID ABX11392 standard; cDNA; 96 BP.
XX AC ABX11392;
XX DT 01-MAY-2003 (first entry)
XX DE Bovine histatin like polypeptide, #5, cDNA.
XX KW Cow; gene; ss; histatin; bovine; salivary secretion; oral cavity;
XX KW non-immune defence system; oral candidosis; gene therapy;
XX KW microbial infection; fungal infection; dental caries; plaque; tartar;
XX KW cystic fibrosis; systemic infection; Candida infection; mastitis;
XX KW fungicide; antibacterial.
XX OS Bos taurus.
XX FH Key
XX CDS Location/Qualifiers
XX FT 1..96
XX FT /*tag= a
XX FT /product= "Histatin like polypeptide"
XX FT /partial
XX FT /note= "No start or stop codon shown"
XX PN US2002164625-A1.
XX PD 07-NOV-2002.
XX PF 19-FEB-2002; 2002US-00079754.
XX PR 23-AUG-1999; 99US-0150330P.
XX PR 29-OCT-1999; 99US-0162701P.
XX PR 22-AUG-2000; 2000US-0064190.
XX PR 27-OCT-2000; 2000US-00699146.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Glenn M, Grigor MR, Molenaar AJ, Davis SR;
XX WPI; 2003-275306/27.
XX P-PSDB; ABG75795.
XX New histatin polynucleotides and polypeptides expressed in bovine
XX tissues, useful for treating bacterial or fungal infections in mammals,
XX e.g. infections of the oral cavity, vagina, urethra, ear or skin, or
XX systemic infections.
XX Claim 1; Page 12; 17pp; English.
XX The invention discloses isolated histatin polynucleotides and
XX polypeptides, which comprise sequences expressed in bovine. Histatins are
XX polypeptides rich and specific to the salivary secretions. They are believed
XX to function as part of the non-immune defence system, particularly in the
XX oral cavity and have promise as therapeutic agents in humans with oral
XX candidosis. Also disclosed are compositions comprising the histatin
XX polypeptide or polynucleotide, and at least one component consisting of
XX physiological or pharmaceutical carriers or immunostimulants. The
XX histatin polynucleotide, polypeptide, or the cosmetic composition
XX comprising the polypeptide, is useful for treating (e.g. gene therapy) a
XX disorder in a mammal, particularly microbial or fungal infections. The
XX histatin polynucleotide is also useful in genome mapping, physical
XX mapping or in the positional cloning of genes. Specifically, the
XX polypeptide or polynucleotide is useful for treating fungal or bacterial
XX infections of the oral cavity (e.g. dental caries, plaque or tartar),
XX vagina, urethra, ear, skin, respiratory tract (e.g. cystic fibrosis,
XX caused by Pseudomonas aeruginosa), mucosa or eye, as well as for treating
XX systemic infections such as systemic Candida infection. The polypeptide
XX or polynucleotide is also useful for veterinary applications e.g. for
XX treating mastitis. The sequence presented is a cDNA encoding a bovine
XX histatin like polypeptide
XX Sequence 96 BP; 33 A; 25 C; 10 G; 28 T; 0 U; 0 Other;
SQ

Query Match 14.4%; Score 87; DB 7; Length 96;
Best Local Similarity 94.7%; Pred. No. 2e-09;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 265 TTTCACAAATACAGCCATATCAAGATATCCACTAAATATCTCTCGGTATCCATTT 324
DB 1 TTTCACAAATACAGCCATATCAAGATATCCACTAAATATCTCTCGGTATCCATTT 60
QY 325 CCTTAAATGCTGCTTAGTAACACAGGACATGAT 359
DB 61 TCTTAAATGCTGCTTACCAACTACAGGACATGAT 95
RESULT 8
AAV89526
ID AAV89526 standard; cDNA; 357 BP.
XX AC AAV89526;
XX DT 15-FEB-1999 (first entry)
XX DE EST clone CP294.
XX KW Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
XX KW tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
XX KW receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
XX KW gene therapy; ss.
XX OS Homo sapiens.
XX PN WO9845436-A2.
XX PD 15-OCT-1998.
XX PF 10-APR-1998; 98WO-US006955.
XX PR 10-APR-1997; 97US-00838821.
XX PA (GENY) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
XX PI Spaulding V, Agostino MJ;
XX WPI; 1999-070077/06.
XX New polynucleotides encoding human secreted proteins - derived from e.g.
XX human blood, kidney, foetal lung, placenta, testes, brain, ovary,
XX pituitary, retina and colon cDNA libraries.
XX Claim 1; Page 245; 618pp; English.
XX The present sequence represents a human expressed sequence tag (EST). The
XX polynucleotide, which is a secreted EST, and the encoded protein are
XX predicted to have useful biological activities which would make them
XX suitable for treating, preventing or ameliorating medical conditions in
XX humans and animals, although no supporting data is given. Suggested
XX activities include nutritional activity, immune stimulating or
XX suppressing activity, haematopoiesis regulating activity, tissue growth
XX activity, activin/inhibin activity, chemotactic/chemokinetic activity,
XX haemostatic and thrombolytic activity, receptor/ligand activity, anti-
XX inflammatory activity, cadherin/tumour invasion suppressor activity,
XX tumour inhibition activity. The polynucleotide may also be useful for
XX gene therapy
XX Sequence 357 BP; 101 A; 74 C; 65 G; 117 T; 0 U; 0 Other;
SQ

Query Match 12.5%; Score 75.4; DB 2; Length 357;
Best Local Similarity 59.4%; Pred. No. 7.6e-07;
Matches 149; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 120 GAATTTTCATCTTTCATGACTGCACTCCACCAATAATGAAGATCTTTATCTTGTCTTCAT 179
DB 48 GACTCTCTCTTGGAGTAAAGGACTCAGCAACTATGAAGTTTGTCTTGTCTTGTAGT 107

```
QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCACTGAAGAGAAACGTCACAGGAA 239
Db 108 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAGAAGACATCATGGGTA 167
QY 240 ACGGAAAAACATCATAGAGGATATTTCAACAATACCGAGCCATATCAACGATATCCACT 299
Db 168 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCGAGATTTCCATTTATGG 221
QY 300 AAATATATCTCTCGCGTATCCATTTCTTAAATGCTGTAGTAATACTACAGGACATGAT 359
Db 222 GGACTGTGGATCAAAATATCTATATGACAATTCATATCTCTTAGTAATCATGGGGCATGAT 281
QY 360 TAGAGAGATTT 370
Db 282 TATAGAGGTTT 292

RESULT 9
ID ACC51062 standard; cDNA; 438 BP.
XX
AC ACC51062;
XX
DT 13-JUN-2003 (first entry)
XX
DE Human Chimera coding sequence.
XX
KW Human; GENSET; therapeutic; therapy; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200294864-A2.
XX
PD 28-NOV-2002.
XX
PF 06-AUG-2001; 2001WO-IB001715.
XX
PR 25-MAY-2001; 2001US-0293574P.
PR 15-JUN-2001; 2001US-0298698P.
PR 29-JUN-2001; 2001US-0302277P.
PR 13-JUL-2001; 2001US-0305456P.
XX
XX (GEST ) GENSET.
XX
PI Bejanin S, Tanaka H;
XX
WPI; 2003-129412/12.
DR P-PSDB; ABR48455.
XX
XX New GENSET polynucleotides and polypeptides, useful for preparing a
PT composition for treating GENSET-related disorders and as reagents in
PT assays to quantitatively determined levels of GENSET expression in
PT biological samples.
XX
PS Claim 1; Page 404-405; 505pp; English.
XX
XX The present invention relates to novel human GENSET coding sequences
CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
CC sequences are useful for preparing a composition for treating GENSET-
CC related disorders. They can also be used as markers for tissues in which
CC the corresponding protein is preferentially expressed, as molecular
CC weight markers on Southern gels, as chromosome markers or tags to
CC identify chromosomes, and as reagents in assays to quantitatively
CC determined levels of GENSET expression in biological samples
XX
SQ Sequence 438 BP; 155 A; 80 C; 60 G; 143 T; 0 U; 0 Other;
XX
Query Match 11.7%; Score 70.4; DB 7; Length 438;
Best Local Similarity 69.9%; Pred. No. 9.3e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 120 GAATTTTCATCTTTCATGCTGGACTCCACCAATATGAAGATCTTTATCTTCTTCAT 179
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Db 50 GACTCTCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTGTCTTGCTTTAGT 109
QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCACTGAAGAGAAACGTCACAGGAA 239
Db 110 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAGAAGACATCATGGGTA 169
QY 240 ACGGAAAAACATCAT 255
Db 170 TAGAAGAAATTCAT 185

RESULT 10
ID ABZ36590 standard; cDNA; 438 BP.
XX
AC ABZ36590;
XX
DT 21-FEB-2003 (first entry)
XX
DE Human GENSET coding sequence SEQ ID 358.
XX
KW Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;
KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
KW inflammatory disease; immune disorder; neuromuscular; toxicity;
KW central nervous system; cardiovascular; gastrointestinal; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200283899-A1.
XX
PD 24-OCT-2002.
XX
PF 18-APR-2001; 2001WO-IB000914.
XX
PR 18-APR-2001; 2001WO-IB000914.
XX
XX (GEST ) GENSET.
XX
PI Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;
XX
WPI; 2003-075548/07.
XX
XX New GENSET polynucleotides and polypeptides, useful for treating heavy
PT metal toxicity, cancer, inflammatory diseases, immune disorders, and the
PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
PT toxicity.
XX
PS Claim 12; Page 478; 735pp; English.
XX
XX The present invention relates to novel GENSET polynucleotides (ABZ36404-
CC ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides
CC and polypeptides are useful in screening and diagnostic assays for
CC abnormal GENSET expression and/or biological activity. They are also
CC useful for screening of compounds for treating or preventing GENSET-
CC related disorders, such as heavy metal toxicity, cancer, inflammatory
CC diseases, immune disorders, and the neuromuscular, central nervous system
CC (CNS), cardiovascular or gastrointestinal effects of the toxicity. The
CC polynucleotides are useful for constructing or expanding chromosome maps
XX
SQ Sequence 438 BP; 151 A; 80 C; 60 G; 145 T; 0 U; 2 Other;
XX
Query Match 11.7%; Score 70.4; DB 7; Length 438;
Best Local Similarity 69.9%; Pred. No. 9.3e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 120 GAATTTTCATCTTTCATGCTGGACTCCACCAATATGAAGATCTTTATCTTGTTCAT 179
Db 50 GACTCTCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTGTCTTGCTTTAGT 109
QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCACTGAAGAGAAACGTCACAGGAA 239
Db 110 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAGAAGACATCATGGGTA 169
```

QY 240 ACGGAAAAAACATCAT 255
 DB 170 TAGAAGAAAAATTCAT 185

 RESULT 11
 ID ABZ36425 standard; cDNA; 438 BP.
 AC ABZ36425;
 XX 21-FEB-2003 (first entry)
 DT Human GENSET coding sequence SEQ ID 22.
 DE Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant;
 KW gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;
 KW inflammatory disease; immune disorder; neuromuscular; toxicity;
 KW central nervous system; cardiovascular; gastrointestinal; gene; ss.
 XX Homo sapiens.
 OS
 XX WO20028398-A1.
 PN 24-OCT-2002.
 XX 18-APR-2001; 2001WO-IB000914.
 XX 18-APR-2001; 2001WO-IB000914.
 XX (GENSET) GENSET.
 XX Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;
 PI WPI; 2003-075548/07.
 DR New GENSET polynucleotides and polypeptides, useful for treating heavy
 XX metal toxicity, cancer, inflammatory diseases, immune disorders, and the
 PT neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
 PT toxicity.
 XX Claim 12; Page 295; 735pp; English.
 PS The present invention relates to novel GENSET polynucleotides (ABZ36404-
 CC ABZ36911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides
 CC and polypeptides are useful in screening and diagnostic assays for
 CC abnormal GENSET expression and/or biological activity. They are also
 CC useful for screening of compounds for treating or preventing GENSET-
 CC related disorders, such as heavy metal toxicity, cancer, inflammatory
 CC diseases, immune disorders, and the neuromuscular, central nervous system
 CC (CNS), cardiovascular or gastrointestinal effects of the toxicity. The
 CC polynucleotides are useful for constructing or expanding chromosome maps
 XX Sequence 438 BP; 153 A; 80 C; 60 G; 143 T; 0 U; 2 Other;
 SQ
 Query Match 11.7%; Score 70.4; DB 7; Length 438;
 Best Local Similarity 69.9%; Pred. No. 9.3e-06;
 Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
 QY 120 GAATTCATCTTCATGACTGCTCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
 DB 50 GACTCTCTCTTGAGTAAAGAGCTCAGCCAACTATGAAGTTTTTGTCTTTAGT 109
 QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239
 DB 110 CTGGCTCTCTGATTTCCATGATTAGGCTGATTCATCAATGAAAAGAGACATCATGGSTA 169
 QY 240 ACGGAAAAAACATCAT 255
 DB 170 TAGAAGAAAAATTCAT 185

 RESULT 12
 ID AAH98658 standard; cDNA; 857 BP.
 AC AAH98658;
 XX 12-OCT-2001 (first entry)
 DT Human EST-derived coding sequence SEQ ID NO: 515.
 DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition; ss.
 XX Homo sapiens.
 OS
 XX WO200154477-A2.
 PN 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-US002687.
 XX 25-JAN-2001; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX WPI; 2001-476164/51.
 DR P-PSDB; AAM23999.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 PT Claim 1; Page 537; 1275pp; English.
 PS The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention
 XX Sequence 857 BP; 231 A; 194 C; 169 G; 263 T; 0 U; 0 Other;
 SQ
 Query Match 11.3%; Score 68.2; DB 4; Length 857;
 Best Local Similarity 65.4%; Pred. No. 3.1e-05;
 Matches 100; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
 QY 120 GAATTCATCTTCATGACTGCTCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
 DB 361 GATTCCTCTCTTGAGTAAAGAGCTCAGCCAACTATGAAGTTTTTGTCTTTAAT 420
 QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239
 DB 421 CTGGCTCTCTGATTTCCATGACTGGAGCTGATTCATCAATGAAAAGAGACATCATGGSTA 480
 QY 240 ACGGAAAAAACATCATAGGATATTTTCAACA 272
 DB 481 TAAAGAAAAATTCATGAAAGACATCATTCACA 513

 RESULT 13
 ID AAA48964 standard; DNA; 552 BP.
 XX

AC AAA48964;
 XX 06-OCT-2000 (first entry)
 XX Human statherin DNA.
 XX Lysine-rich statherin protein; LRSP; acidic phosphoprotein; human;
 KW precipitation inhibitor; autoimmune, inflammatory disorder; AIDS; asthma;
 KW allergy; diabetes mellitus; fungal; bacterial infection; cancer;
 KW leukemia; adenocarcinoma; melanoma; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 73..261
 FT /*tag= a
 FT /product= "Statherin"
 XX WO200024779-A1.
 XX 04-MAY-2000.
 XX 22-OCT-1999; 99WO-US024046.
 XX 23-OCT-1998; 98US-0155209P.
 XX (INCY-) INCYTE PHARM INC.
 XX Tang YT, Corley NC, Guesler KJ, Patterson C;
 XX WPI; 2000-350699/30.
 DR P-PSDB; AAY94527.
 XX Purified polypeptide used for treating or preventing a disorder
 PT characterized by expression or activity of lysine-rich statherin
 PT proteins.
 XX Disclosure; Page 71; 75pp; English.
 XX The present invention relates to human lysine-rich statherin protein
 CC (LRSP) (AAY94526). The cDNA sequence encoding this protein was identified
 CC through analysis of a cDNA library of breast tumour tissue (BRSTNCT14).
 CC The LRSP sequence was found to have homology with the DNA of human
 CC statherin (the present sequence) and human basic histidine-rich protein
 CC (AAY94528). Human statherin is a phosphoprotein that acts as an inhibitor
 CC of precipitation of calcium phosphate salts in the oral cavity. The LRSP
 CC polypeptide and its antagonists may be useful for treating or preventing
 CC disorders associated with the activity of LRSP. Such disorders include
 CC autoimmune/inflammatory disorders (for example AIDS, allergies, asthma,
 CC diabetes mellitus), bacterial and fungal infection and cancers (such as
 CC leukemia, adenocarcinoma, melanoma). Antibodies to LRSP may be useful for
 CC diagnosis of the above disorders
 XX Sequence 552 BP; 172 A; 122 C; 78 G; 180 T; 0 U; 0 Other;
 SQ

Query Match 11.2%; Score 67.6; DB 3; Length 552;
 Best Local Similarity 61.2%; Pred. No. 3.8e-05;
 Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;

Qy 140 GGATCTCACCAATATGAAGATCTTTATCTTGTCTTCATATGGCTCTCATCTAGCCA 199
 Db 59 GAACCCAGCCAACTATGAGTCTCTTCTTGTCTTCATCTTGTCTCTCATCTAGTTCCA 118
 Qy 200 TGATTAGGCTGATCTCTGAAGAGAAACGTCACAGGAAACCGGAAACATCATAGAG 259
 Db 119 TGATTGGAGCTGATCTCTGAGAGAAATTTTTCGCTAGAAATTTGGAAGATTCGGTTATG 178
 Qy 260 GATA-----TTTTTCAACAATACAGCCATATCAAGATATCCACTAAATTCCTCCCTG 313
 Db 179 GGTATGCCCTTATCAGCCAGTCTTCAAGAACACACCATATACCCACACCATACACAC 238
 Qy 314 CGT---ATCCATTTCTTAAATGCTGCTTAGTAACCTACAGGACATGATTAGAGATTT 370

Db 239 AATACCAACAATATACCTTTTAAATATCATCATCACTCACTCACTCACTCACTCACT 298
 RESULT 14
 ADE40261
 ID ADE40261 standard; cDNA; 678 BP.
 XX ADE40261;
 AC ADE40261;
 XX 29-JAN-2004 (first entry)
 DT Human NOV38a cDNA - SEQ ID 167.
 XX
 DE
 XX NOVX; cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW anti-diabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
 KW antiparkinsonian; antiasthmatic; gynaecological; cardiomyopathy;
 KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
 KW multiple sclerosis; graft-versus-host disease; Alzheimer's; Parkinson's;
 KW asthma; fertility disorder; vaccine; gene therapy; chromosome mapping;
 KW tissue typing; human; NOV; ss; gene.
 XX
 XX Homo sapiens.
 OS
 XX WO2003064589-A2.
 XX 07-AUG-2003.
 XX 02-AUG-2002; 2002WO-US024483.
 XX 02-AUG-2001; 2001US-0309501P.
 PR 03-AUG-2001; 2001US-0310291P.
 PR 07-AUG-2001; 2001US-0310544P.
 PR 08-AUG-2001; 2001US-0310951P.
 PR 09-AUG-2001; 2001US-0311292P.
 PR 13-AUG-2001; 2001US-0311979P.
 PR 16-AUG-2001; 2001US-0312892P.
 PR 17-AUG-2001; 2001US-0313201P.
 PR 17-AUG-2001; 2001US-0313415P.
 PR 20-AUG-2001; 2001US-0313643P.
 PR 20-AUG-2001; 2001US-0313702P.
 PR 21-AUG-2001; 2001US-0314031P.
 PR 23-AUG-2001; 2001US-0314466P.
 PR 28-AUG-2001; 2001US-0315403P.
 PR 29-AUG-2001; 2001US-0315853P.
 PR 17-SEP-2001; 2001US-0322716P.
 PR 21-SEP-2001; 2001US-0323994P.
 PR 14-DEC-2001; 2001US-0340233P.
 PR 05-FEB-2002; 2002US-0354591P.
 PR 19-MAR-2002; 2002US-0365478P.
 PR 19-APR-2002; 2002US-0373814P.
 PR 19-APR-2002; 2002US-0373825P.
 PR 19-APR-2002; 2002US-0373989P.
 PR 23-APR-2002; 2002US-0374632P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 01-AUG-2002; 2002US-00210172.
 XX (CURA-) CURAGEN CORP.
 XX Kekuda R, Miller CE, Patturajan M, Pena CEA, Rieger DK;
 PI Shinkets RA, Zerhusen BD, Li L, Ji W, Padigaru M, Casman SU;
 PI Voss EZ, Boldog FL, Gorman L, Leite MW, Vernet CAM, Anderson DW;
 PI Guo X, Zhong M, Gerlach VL, Hjalt T, Rastelli L, Spytek KA;
 PI Edinger SR, Ellerman K, Malyankar UM, Macdougall JR, Stone DJ;
 PI Alsobrook JP, Lepley DW, Burgess CE, Majumder K, Wolenc AR;
 PI Smithson G;
 XX WPI; 2003-663472/62.
 DR P-PSDB; ADE40262.
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Claim 20; SEQ ID NO 167; 560pp; English.
 XX PS
 XX CC The invention relates to a novel NOVX polypeptide. The polypeptide-of the
 CC invention demonstrates cardiant, antiarteriosclerotic, hypotensive,
 CC cyostatic, anorectic, antidiabetic, immunosuppressive, anti-HIV,
 CC neuroprotective, nootropic, antiparkinsonian, antiasthmatic and
 CC gynaeological activities and may be useful in diagnosing, treating or
 CC preventing NOVX-associated disorders including cardiomyopathy,
 CC atherosclerosis, hypertension, cancer, obesity, diabetes, Parkinson's
 CC sclerosis, graft-versus-host disease, Alzheimer's disease, Parkinson's
 CC disease, asthma or fertility disorders. Furthermore, the polypeptides may
 CC be utilised as vaccines whilst the nucleic acids may be used as
 CC hybridisation probes, in gene therapy, chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV cDNA of the invention.
 XX
 XX SQ Sequence 678 BP; 190 A; 151 C; 137 G; 200 T; 0 U; 0 Other;

Query Match 11.2%; Score 67.6; DB 9; Length 678;
 Best Local Similarity 61.2%; Pred. No. 4e-05;
 Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;
 140 GGACTCCACCAATATGAAGATCTTTATCTTTGTTTCATTATGGCTCTCATCTAGCCA 199
 Db 256 GAACCCAGCCAACTATGAGTTCCTTCTTTGCTTCACTTGGCTCTCATGGTTTCCA 315
 QY 200 TGATTAGAGCTGATCTATCTGAGAGAAAGCTCACAGGAACGGAAACATCATAGAG 259
 Db 316 TGAATTGAGCTGATCTATCTGAGAGAAATTTTGGCTGAAATGGAAGATTCGGTTATG 375
 QY 260 GATA-----TTTTCACAAATACAGGCATATCAACGATATCCACTAAATATTCCTCTG 313
 Db 376 GGTATGGCCCTTATGACCGAGTTCAGAACACCACTATACCCACCAACCAACAC 435
 QY 314 CGT---ATCCATTTCCTTAAATCTGTTAGTAACTACAGGACATGATTAGAGATTT 370
 Db 436 AATACCAACAATATACCTTTTAAATATCATCATGTAACCTGCAGGACATGATTATTGAGGCTT 495

RESULT 15
 ADB63039
 ID ADB63039 standard; cDNA; 1584 BP.
 AC ADB63039;
 XX
 XX DT 04-DEC-2003 (first entry)
 XX DE Human cDNA encoding clone SALGL10001070.
 XX KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
 KW tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KW osteoporosis; neurological disease; cancer; tumour.
 XX
 XX OS Homo sapiens.
 XX
 XX FH Key Location/Qualifiers
 XX CDS 89..997
 XX FT /tag= a
 XX FT /product= "Clone SALGL10001070 protein"
 XX
 XX PN EP1308459-A2.
 XX
 XX PD 07-MAY-2003.
 XX
 XX PF 28-MAR-2002; 2002EP-00007401.
 XX
 XX PR 05-NOV-2001; 2001JP-00379298.
 XX 25-JAN-2002; 2002US-00350978.
 XX
 XX (HELI-) HELIX RES INST.
 XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-450961/43.
 DR P-PSDB; ADB65009.
 XX
 XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 PS Claim 1; Page: 222pp; English.
 XX
 XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence
 CC data for this patent is not represented in the printed specification, but
 CC is based on sequence information supplied by the European Patent Office.
 XX
 XX Sequence 1584 BP; 526 A; 298 C; 331 G; 429 T; 0 U; 0 Other;

Query Match 11.2%; Score 67.6; DB 9; Length 1584;
 Best Local Similarity 61.2%; Pred. No. 4.6e-05;
 Matches 147; Conservative 0; Mismatches 84; Indels 9; Gaps 2;
 QY 140 GGACTCCACCAATATGAAGATCTTTATCTTTGTTTCATTATGGCTCTCATCTAGCCA 199
 Db 1083 GAACCCAGCCAACTATGAGTTCCTTGTCTTTCCTTCACTTGGCTCTCATGGTTTCCA 1142
 QY 200 TGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAACGGAAACCAATCATAGAG 259
 Db 1143 TGAATTGAGCTGATTCATCTGAAGAGAAATTTTGGCTGAAATTCGGTTATG 1202
 QY 260 GATA-----TTTTCAACAATACAGCCATATCAACGATATCCCACTAAATATCTCTCTG 313
 Db 1203 GGTATGGCCCTTATCAGCCAGTTCCAGAAACCACTATACCCACCAACCAACAC 1262
 QY 314 CGT---ATCCATTTCCTTAAATGCTGCTTAGTAACTACAGGACATGATTAGAGATTT 370
 Db 1263 AATACCAACAATATACCTTTTAAATATCATCATGTAACCTGCAGGACATGATTATTGAGGCTT 1322

Search completed: August 15, 2004, 21:45:07
 Job time : 355 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 21:39:53 ; Search time 73 Seconds
(without alignments)

4591.648 Million cell updates/sec

Title: US-10-079-754A-4

Perfect score: 604
Sequence: 1 gaagatttcagttctata.....tatcaagcataaaaaaaa 604

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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 - 2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
 - 3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42.4	7.0	640681	4	US-09-790-988-1
C 2	42.2	7.0	640681	4	US-09-790-988-1
C 3	41.8	6.9	11131	4	US-10-204-708-28
C 4	41.4	6.9	5501	4	US-10-204-708-38
C 5	41.4	6.9	19513	4	US-10-204-708-39
C 6	41.2	6.8	1864	4	US-09-468-265-4
C 7	41	6.8	750	4	US-09-023-655-197
C 8	41	6.8	5152	4	US-10-204-708-74
C 9	41	6.8	11469	4	US-09-367-895-29
C 10	41	6.8	11478	3	US-08-981-803-29
C 11	41	6.8	11478	3	US-08-983-440-29
C 12	40.8	6.8	6152	3	US-08-973-462-1
C 13	40.4	6.7	465	6	549550-9
C 14	40.4	6.7	465	6	549550-7
C 15	40.2	6.7	6152	3	US-08-973-462-1
C 16	40	6.6	789	4	US-09-702-705-214
C 17	40	6.6	789	4	US-09-736-457-214
C 18	40	6.6	789	4	US-09-614-1245-214
C 19	40	6.6	789	4	US-09-671-325-214
C 20	40	6.6	789	4	US-09-589-184-214
C 21	40	6.6	6583	4	US-10-204-708-26
C 22	40	6.6	7664	4	US-10-204-708-84
C 23	39.8	6.6	4185	4	US-09-417-485D-7
C 24	39.8	6.6	6107	4	US-09-482-273-47
C 25	39.8	6.6	10640	4	US-09-417-485D-5
C 26	39.6	6.6	10640	4	US-09-417-485D-5
C 27	39.4	6.5	128779	4	US-09-457-855A-38

C 28	39.2	6.5	832	4	US-09-621-976-2813
C 29	39	6.5	832	4	US-09-621-976-2813
C 30	39	6.5	19124	2	US-08-487-826B-13
C 31	39	6.5	1664976	4	US-08-916-421B-1
C 32	38.8	6.4	19124	2	US-08-487-826B-13
C 33	38.4	6.4	510	4	US-09-543-681A-2705
C 34	38.4	6.4	989	3	US-08-817-926-2
C 35	38.4	6.4	3562	3	US-08-817-926-19
C 36	38.4	6.4	202001	4	US-09-734-674-3
C 37	38	6.3	1897	1	US-08-184-632-1
C 38	38	6.3	10467	4	US-10-204-708-2
C 39	37.8	6.3	766431	4	US-09-751-389-3
C 40	37.6	6.2	5535	4	US-10-204-708-18
C 41	37.4	6.2	5340	4	US-09-627-122-21
C 42	37.4	6.2	5852	1	US-07-867-106-2
C 43	37.2	6.2	5360	4	US-10-204-708-65
C 44	37	6.1	840	4	US-09-134-001C-1831
C 45	37	6.1	2621	2	US-08-553-619B-8

ALIGNMENTS

RESULT 1

US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match	7.0%;	Score 42.4;	DB 4;	Length 640681;
Best Local Similarity	47.4%;	Fred. No. 1.8;	Mismatches 141;	Indels 0;
Matches 127;	Conservative 0;			Gaps 0;
QY	39	TGTAATTACAAAAACAATGAAGGATTTCAAGGTATTTAAACACAGCAGTCTTTCTAGCAA	98	
Db	518530	TATTAATAATTAGAAAAACAACATAAATTAATGTTTATAGAAAAGGAAAACTCCTATTAG	518589	
QY	99	AGAACATCTCTGGAAGCATCAGATTTTCATCTTCATGCTGGACTCCACCAATATGAA	158	
Db	518590	AGTAATACAGAAAAAGTATGCTAGTCTATTTATATATATATATTTAAAAAATAATGCA	518649	
QY	159	GATCTTTTCTTTGCTTCATTTATGCTCTCATCTAGCCATGATTAGAGCTGATTCTATC	218	
Db	518650	AAAAATTTTCTAGTAATTTATAAGACAGAAAAATAAATATTGTTCTCCGAATTT	518709	
QY	219	TGAAGAGAAACGTCACAGGAAACGGAAAAACATCATAGAGATATTTTCAACAATACCA	278	
Db	518710	TTATATCCATCAAGTGAAGATAAAAAAAGAAATATTTTGAATATTTCTGTAATTTACGA	518769	
QY	279	GCCATATCAAGATATCCACTAAATAT	306	
Db	518770	ACTATATCCAAATTTCAATATAAGAT	518797	

RESULT 2

US-09-790-988-1/c

```
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: SHIGENOBU, HIDEMI
; APPLICANT: WATANABE, MASAHIRA
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchneza sp.
; US-09-790-988-1

Query Match      7.8%; Score 42.2; DB 4; Length 640681;
Best Local Similarity 47.5%; Pred. No. 2; Mismatches 138; Indels 0; Gaps 0;
Matches 125; Conservative 0;

QY 246 AAAAAATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTA 305
DB 220824 AAAAAATCATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTAAATTA 305

QY 306 TCCTCTCGGTATCCATTTCCCTTAAATGCTGTAGTAACTACAGAGCATGATTAGAGA 365
DB 220764 TTACGTTGAGAAATTAATGCACTAGTGTGTTCAATTAATAACATCATCGTATTCCTAGTAGC 220705

QY 366 GATTTTTCAGATGATTTTCCCTACTCTTTCTGTGTGTTGAAACCAATCTTTCAAATGA 425
DB 220704 TGTTTTCATATCAAAATTCGATTTTCTACTTTTGTGAGCGTTTCTATTGCTTTT 220645

QY 426 ATAAACAAAGAAAGAAATTAATCAAGTCAAGTGTGTCACAAACATATCTTGGAAATCAAAATA 485
DB 220644 GTTACCAGGAATGCTCGATGCTTCAATTAAGAACTAATCCTAATTTTTCATCATATGA 220585

QY 486 TCAATATTTTAAACATAAAT 508
DB 220584 ACAATTTTATGACGCAAAAAT 220562

RESULT 3
US-10-204-708-28/c
; Sequence 28, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 28
; LENGTH: 11131
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-204-708-28

Query Match      6.9%; Score 41.4; DB 4; Length 5501;
Best Local Similarity 49.8%; Pred. No. 0.82;
Matches 105; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 300 AAATTATCTCTCGGTATCCATTTCCCTTAAATGCTGCTTAGTAACTACAGGATCATGAT 359
DB 2041 AATTATAAACTAATCCCAATCCCTACATTTTAACTTTTAAATTTCAAAATATAA 1982
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QY 360 TAGAGAGATTTTTCACAAATGATTTTCCCTACTCTTTCTGTGTGTGTTGAAACCATCTTTC 419
Db 1981 TACATTTTATTTTAAAAAATAAATTTCTTCAAAAACAAAATAATCTAAATATCACCTAAA 1922
QY 420 AATGATATAAACAAGAAAAAATAATCTCAAGTAGTTGCAACACATATCTTGGAAAT 479
Db 1921 ATAAAAATTAACAAAAAATAATATACAAAAAATAATCAAAATCATATATATAA 1862
QY 480 CAAATATCAATTTTAAAAACATAAATAATGA 510
Db 1861 TAAAAATATAAANAATAAATAAATAATCA 1831

RESULT 5
US-10-204-708-39/c
; Sequence 39, Application US/10204708
; Patent No. 667731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BEBLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 39
; LENGTH: 19513
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-39

Query Match 6.9%; Score 41.4; DB 4; Length 19513;
Best Local Similarity 46.9%; Pred. No. 1.2; Mismatches 146; Indels 0; Gaps 0;
Matches 129; Conservative 0;
QY 227 AACGTCACAGGAACCGAAAAACATCATAGAGGATATTTTCAACAATACCGCCATATC 286
Db 9628 AACTACTCAAAAACACTACATAAARAATCGTTAAACCTTAAAAACAAAATTACAATA 9569
QY 287 AACGATATCCACTAAATATCTCTCGGTATCCATTTCTTTAAATGCTGCTTAGTAAC 346
Db 9568 AACCAAAATCGCACCACTATCTCCAACTTAAATAACAAAAACAAAACCTCGTCTCAAAA 9509
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Db 9508 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9449
QY 407 AAAACCATCTTTCAATGAATAAACAAGAAAAAATAATCAGTCAAGTAGTTGCAACAC 466
Db 9448 AACCAACATTTTCAATAATTTCAACCAAAAAAATAAATAAATAAATAAATAAATAA 9389
QY 467 ACATCTTGGATCAATATCAATATTTTAAACA 501
Db 9388 ACTTAAATAAACAATAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9354

RESULT 6
US-09-468-265-4

; Sequence 4, Application US/09468265
; Patent No. 637928
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M
; APPLICANT: Cullen, Daniel
; APPLICANT: Gray, Gregory L
; APPLICANT: Hayenga, Kirk J
; APPLICANT: Lawlis, Virgil B
; TITLE OF INVENTION: Heterologous Polypeptides Expressed in Filamentous Fungi, Process
; TITLE OF INVENTION: Making Same and Vectors for Making Same
; FILE REFERENCE: A-42903-5
; CURRENT APPLICATION NUMBER: US/09/468,265
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 08/484,384
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/284,942
; PRIOR FILING DATE: 1994-08-02
; PRIOR APPLICATION NUMBER: 07/413,010
; PRIOR FILING DATE: 1989-09-25
; PRIOR APPLICATION NUMBER: 07/163,219
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 06/882,224
; PRIOR FILING DATE: 1986-07-07
; PRIOR APPLICATION NUMBER: 06/771,374
; PRIOR FILING DATE: 1985-08-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Emericella nidulans
US-09-468-265-4

Query Match 6.8%; Score 41.2; DB 4; Length 1864;
Best Local Similarity 46.3%; Pred. No. 0.68;
Matches 136; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 221 AAGAGAAACGTCACAGGAACCGAAAAACATCATAGAGGATATTTTCAACAATACCGAC 280
Db 1224 AAGATATCTAGCCAGGCTAGACAATAATACTTAAAAATATATAAAAAATAGCTACTAA 1283
QY 281 CATATCAAGGATATCCATTAATTTCTCTCGGTATCCATTTCTTAAATGCTGCTT 340
Db 1284 AACTGAATAATTAAGAAGATAGTATTTATCTTAAGTAACTTAAATCTTAGTAATCTA 1343
QY 341 AGTAACACAGGACATGATTAGAGAGATTTTTCACAATGATTTTTCCTACTCTTTCTGT 400
Db 1344 AAGATTTTAAATTAATTAATAAATAATATAATAATAGTTGACCTTGAACTGTTACTAAA 1403
QY 401 GTGTTGAAAACCATCTTTCAAATGAATAAACAAGAAAAAATAATCAGTCAAGTAGTTG 460
Db 1404 CTTTATTATAATTTATTATTAATTAATACTAAGCTAAGCTAAGCTAAGCTAAGCTA 1463
QY 461 CACAACACATCTTGAATCAATATCAATATTTTAAAAACATAAATAATGATAGT 514
Db 1464 TAAAAATAGCTAGAGATTAATAAGCTCTATAAAAAATTTTAAAGATTATT 1517

RESULT 7
US-09-023-655-197/c
; Sequence 197, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO

QY 428 AAAACAAGAAAAAATCAGTCAAGTAGTGGACACACATACCTTGGAAATCAATATC 487
Db 11312 AAAACAATGAAGAAATCAATAGAAAGAGAGAAATTTTCATCTCATTTGAAAGCGAA 11253
QY 488 AATATTTTAAACATATATGATAGTCTCTGAACTATATGTAATGGTTTCTACTTTCTTT 547
Db 11252 AATCTACTAGAGAGATGATGATGAACTCTTGAACTTTCAATAGTGACACCCCTTCGTT 11193
QY 548 TCTCT 552
Db 11192 CTACT 11188

RESULT 10
US-08-981-803-29/c
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: POULSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981,803
; EARLIER FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12
; EARLIER APPLICATION NUMBER: 9514435.8
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-29

Query Match 6.8%; Score 41; DB 3; Length 11478;
Best Local Similarity 51.4%; Pred. No. 1.3;
Matches 95; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 368 TTTTTCACATGATTTTCTCTACTCTTCTGTTGTGTTGAAACCATCTTTCAAATGAAT 427
Db 11381 TTGACATCTTTCTGTTATTAATTTCTTTTCAATACACACCAATGAAG 11322
QY 428 AAAACAAGAAAAAATCAGTCAAGTAGTGGACACACATACCTTGGAAATCAATATC 487
Db 11321 AAAACAATGAAGAAATCAATAGAAAGAGAGAAATTTTCATCTCATTTGAAAGCGAA 11262
QY 488 AATATTTTAAACATATATGATAGTCTCTGAACTATATGTAATGGTTTCTACTTTCTTT 547
Db 11261 AATCTACTAGAGAGATGATGATGAACTCTTGAACTTTCAATAGTGACACCCCTTCGTT 11202
QY 548 TCTCT 552
Db 11201 CTACT 11197

RESULT 11
US-08-983-440-29/c
; Sequence 29, Application US/08983440
; Patent No. 623122
; GENERAL INFORMATION:
; APPLICANT: POULSEN, Peter
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2003
; CURRENT APPLICATION NUMBER: US/08/983,440
; CURRENT FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 9514437.4
; EARLIER FILING DATE: 1995-07-14
; EARLIER APPLICATION NUMBER: PCT/EP96/03053
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(11478)
; OTHER INFORMATION: B stands for G or C or T/U
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(11478)
; OTHER INFORMATION: R stands for G or A
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(11478)
; OTHER INFORMATION: K stands for G or T/U
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(11478)
; OTHER INFORMATION: W stands for A or T/U
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)..(11478)
; OTHER INFORMATION: M stands for A or C
US-08-983-440-29

Query Match 6.8%; Score 41; DB 3; Length 11478;
Best Local Similarity 51.4%; Pred. No. 1.3;
Matches 95; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 368 TTTTTCACATGATTTTCTCTACTCTTCTGTTGTGTTGAAACCATCTTTCAAATGAAT 427
Db 11381 TTGACATCTTTCTGTTATTAATTTCTTTTCAATACACACCAATGAAG 11322
QY 428 AAAACAAGAAAAAATCAGTCAAGTAGTGGACACACATACCTTGGAAATCAATATC 487
Db 11321 AAAACAATGAAGAAATCAATAGAAAGAGAGAAATTTTCATCTCATTTGAAAGCGAA 11262
QY 488 AATATTTTAAACATATATGATAGTCTCTGAACTATATGTAATGGTTTCTACTTTCTTT 547
Db 11261 AATCTACTAGAGAGATGATGATGAACTCTTGAACTTTCAATAGTGACACCCCTTCGTT 11202
QY 548 TCTCT 552
Db 11201 CTACT 11197

RESULT 12
US-08-973-462-1
; Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1

Query Match 6.8%; Score 40.8; DB 3; Length 6152;
Best Local Similarity 53.0%; Pred. No. 1.2;
Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY	420	AAATGAATATAAACCAAGAAAAAATAATCAGTCAAGTAGTTGCACACACATACTCTGGAAT	479
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QY	480	CAAAATATCAATATATTTTAAAAACATATAATGAATAGTCTCTGAACATATGTAATCGTTTCTTA	539
Db	369	TATATATATATATATATATATATATATATATTTTATTTTATTTATTTATTTTATTTTATTTT	428
QY	540	CTTTCTTTCTCTGTCACTTACCATGCATGCTTAATAAATGAT	583
Db	429	TATTTATCTTTTATGTCATATAACCAAGAGCTTGCAAAAAAAT	472

RESULT 13
5496550-9
; Patent No. 5496550
; APPLICANT: WALLACH, MICHAEL; FUGATSCH, THERA; MENCHER, DAVID
; TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
; OOCYSTS FROM A NEWBORN CHICK

	Query Match	6.7%	Score 40.4	DB 6	Length 465
	Best Local Similarity	51.7%	Prod. No. 0.71		
	Matches	92	Conservative 0	Mismatches 86	Indels 0
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QY	485	ATCAATATTTTAAAA	CATAATATGATAGTCT	CGAACTATGTAAT	TGGTTCTTCTACTTC 544
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QY	545	TTTTCTCTGTCAC	TTCACATGCATGCT	TATTAATAATTGAT	CTCTCAAGCATAAAAAA 602
Db	269	GTGCTTTGTGATTC	ATGTCATGCATGAT	TTCCTTCAAAAAG	CCGCGCAAAAATAAA 326

RESULT 14
5496550-7
; Patent No. 5496550
; APPLICANT: WALLACH, MICHAEL; PUGATSCH, THEA; MENCHER, DAVID
; TITLE OF INVENTION: METHOD OF REDUCING THE OUTPUT OF EIMERIA
; OOCYSTS FROM A NEWBORN CHICK
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/108,763
; FILING DATE: 17-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 642,219
; FILING DATE: 16-JAN-1991
; APPLICATION NUMBER: 310,603
; FILING DATE: 14-FEB-1989
; APPLICATION NUMBER: 155,245
; FILING DATE: 12-FEB-1988
; APPLICATION NUMBER: 896,611
; FILING DATE: 14-AUG-1986

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;SEQ ID NO:7:
;      LENGTH: 466
5496550-7

Query Match      6.7%; Score 40.4; DB 6; Length 466;
Best Local Similarity 51.7%; Fred: No. 0.71; 86; Indels 0; Gaps 0
Matches 92; Conservative 0; Mismatches 0;

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Db 150 AAGCAAGAAACACCTCTTATAGACATGATGAGTAAATTAACACATAATAATTAATA 209
Qy 485 ATCAATATTTTAAAAACATAAATAATGATAGTCTCTGAACATGTAATGGTTCTACTTTC 544
Db 210 ATAAATAAATAAATAATATAATTTTATTTATTTATTTATTTATTTATTTG 269
Qy 545 TTTTCTCTGCTCACTTTACCATCGATGCTTAATAATTCATCTCAAGCATAAAAAAA 602
Db 270 GGTGCTTTGTGATTCATGTCATGCAATTCCTTCAAAAAGCGCGCAAAAAATAA 327

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RESULT 15
US-08-973-462-1/c
; Sequence 1, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 0660-0125-0 PCT
; CURRENT APPLICATION NUMBER: US/08/973,462B
; CURRENT FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: PCT/FR96/00894
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: FR 95/07007
; EARLIER FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1

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Query Match	6.7%;	Score 40.2;	DB 3;	Length 6152;
Best Local Similarity	56.4%;	Pred. No. 1.6;		
Matches	75;	Conservative	0;	Mismatches 58; Indels 0; Gaps 0
QY	420	AAATCAATAAACAAGAAAAAATTCAGTCAGTAGTTGCACACACATACTTCGAAT	479	
Db	440	AAAAAGATATATAAAAAAATAATAATAAATAAAAAATAATATATATATA	381	
QY	480	CAAAATACAAATATTTTAAACATAATAATCATAGTCTCTCGAATCTATGTAATTCGTTCTTA	539	
Db	380	TAGTTGATTTTTTTTTT	321	
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Db	320	TTTTTTTTTTTT	308	

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Job time : 77 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 21:45:13 ; Search time 386 Seconds
(without alignments)
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Perfect score: 604
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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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2	465.4	77.1	505	14	US-10-079-754A-1		Sequence 1, Appli
3	448.2	74.2	585	14	US-10-079-754A-2		Sequence 2, Appli
4	423.4	70.1	525	14	US-10-079-754A-6		Sequence 6, Appli
5	238.4	39.5	267	14	US-10-079-754A-15		Sequence 15, Appli
6	238.4	39.5	267	14	US-10-079-623-200		Sequence 200, App
7	115	19.0	869	14	US-10-079-754A-3		Sequence 3, Appli
8	87	14.4	96	14	US-10-079-754A-5		Sequence 5, Appli
9	70.4	11.7	438	10	US-09-992-600A-5		Sequence 5, Appli
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Sequence 35, Appl
Sequence 739, App
Sequence 236, App
Sequence 74, Appl

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US-10-240-589C-74

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51 8.4 12578 13
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49.4 8.2 15994 15
49.2 8.1 13131 17
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47.8 7.9 6782 15
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45

ALIGNMENTS

RESULT 1
US-10-079-754A-4
; Sequence 4, Application US/10079754A
; Publication No. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-4

Query Match 100.0%; Score 604; DB 14; Length 604;
Best Local Similarity 100.0%; Pred. No. 4.9e-128;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGTATTTTCAGTTCTATAAAGATCTCATACGTGATGTATTCACAAAACAAATGAA 60
Db 1 GAAGTATTTTCAGTTCTATAAAGATCTCATACGTGATGTATTCACAAAACAAATGAA 60

QY 61 GGATTTCAAGGTATTTAAACACAGCAGTCTTTCTAGCAAAACATCTCTGAAGCATCAG 120
 DB 61 GGATTTCAAGGTATTTAAACACAGCAGTCTTTCTAGCAAAACATCTCTGAAGCATCAG 120
 QY 121 AATTTTCATCTTTTCATGACTGGACTCCCAACAAATATGAAGATCTTTTATCTTTTGTCTTCATT 180
 DB 121 AATTTTCATCTTTTCATGACTGGACTCCCAACAAATATGAAGATCTTTTATCTTTTGTCTTCATT 180
 QY 181 ATGCTCTCATCTCTAGCATGATTAGAGCTGATTCATCTCTGAAGAGAAAGCTCAACAGAA 240
 DB 181 ATGCTCTCATCTCTAGCATGATTAGAGCTGATTCATCTCTGAAGAGAAAGCTCAACAGAA 240
 QY 241 CGGAAAAAATCATATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTA 300
 DB 241 CGGAAAAAATCATATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACTA 300
 QY 301 AATTATCTCTCTGGTATCCATTTCTTAAATGCTGCTTAGTAATCAACAGGATGATT 360
 DB 301 AATTATCTCTCTGGTATCCATTTCTTAAATGCTGCTTAGTAATCAACAGGATGATT 360
 QY 361 AGAGAGATTTTTCACAATGATTTTCTCTACTCTTTCTGTTGTTGAAACCACTTTTCA 420
 DB 361 AGAGAGATTTTTCACAATGATTTTCTCTACTCTTTCTGTTGTTGAAACCACTTTTCA 420
 QY 421 AATGAATAAACAAAGAAAAAATCAGTCAAGTAGTTCGCAACACATATCTTGGAAATC 480
 DB 421 AATGAATAAACAAAGAAAAAATCAGTCAAGTAGTTCGCAACACATATCTTGGAAATC 480
 QY 481 AATATCAATATTTTAAACATATATGATGCTCTGAACTATGTAATGTTTCTTAC 540
 DB 481 AATATCAATATTTTAAACATATATGATGCTCTGAACTATGTAATGTTTCTTAC 540
 QY 541 TTTCTTTTCTCTGCTACCTACCATGCTTAAATAAATGATCTATCAAGCATATAAAAA 600
 DB 541 TTTCTTTTCTCTGCTACCTACCATGCTTAAATAAATGATCTATCAAGCATATAAAAA 600
 QY 601 AAAA 604
 DB 601 AAAA 604

RESULT 2

US-10-079-754A-1
 ; Sequence 1, Application US/10079754A
 ; Publication No. US20020164625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Molenaar, Adrian J.
 ; APPLICANT: Davis, Stephen R.
 ; TITLE OF INVENTION: Compositions Isolated from Bovine
 ; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
 ; FILE REFERENCE: 11000.1068
 ; CURRENT APPLICATION NUMBER: US/10/079,754A
 ; PRIOR FILING DATE: 2002-02-19
 ; CURRENT APPLICATION NUMBER: US 09/699,146
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60,162,701
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 09/644,190
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: US 60,150,330
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 505
 ; TYPE: DNA
 ; ORGANISM: Bovine
 US-10-079-754A-1

Query Match

77.1%; Score 465.4; DB 14; Length 505;

Best Local Similarity 99.8%; Pred. No. 2.1e-96;
 Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 138 CTGACTCCCAACAAATATGAAGATCTTTTATCTTTGCTTCTTATATGCTCTCATCTAGC 197
 DB 28 CAGGACTCCCAACAAATATGAAGATCTTTTATCTTTGCTTCTTATATGCTCTCATCTAGC 87
 QY 198 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGCGAAACAAATCATAG 257
 DB 88 CATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAAACGCGAAACAAATCATAG 147
 QY 258 AGGATATTTTCAACAATACAGCCATATCAACGATATCCACTAAATATCTCTCTCGGTA 317
 DB 148 AGGATATTTTCAACAATACAGCCATATCAACGATATCCACTAAATATCTCTCTCGGTA 207
 QY 318 TCCATTTCTTTAAATGCTGTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 377
 DB 208 TCCATTTCTTTAAATGCTGTTAGTAACTACAGGACATGATTAGAGAGATTTTTCACAA 267
 QY 378 TGATTTTCTTACTCTTTCTGTTGTTGAAACCACTTTTCAAAATGAATAAACAAGA 437
 DB 268 TGATTTTCTTACTCTTTCTGTTGTTGAAACCACTTTTCAAAATGAATAAACAAGA 327
 QY 438 AAAAAAATCAGTCAAGTAGTTCGCAACACATATCTTGGAAATCAAAATCAATATTTTAA 497
 DB 328 AAAAAAATCAGTCAAGTAGTTCGCAACACATATCTTGGAAATCAAAATCAATATTTTAA 387
 QY 498 AACATAAATATGATGATCTCTGAACATATGTAATGTTTCTTACTTTTCTCTGTCTAC 557
 DB 398 AACATAAATATGATGATCTCTGAACATATGTAATGTTTCTTACTTTTCTCTGTCTAC 447
 QY 558 TTACATGATGCTTTAAATAAATGATCTATCAAGCATATAAAAAA 604
 DB 448 TTACATGATGCTTTAAATAAATGATCTATCAAGCATATAAAAAA 494

RESULT 3

US-10-079-754A-2
 ; Sequence 2, Application US/10079754A
 ; Publication No. US20020164625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glenn, Matthew
 ; APPLICANT: Molenaar, Adrian J.
 ; APPLICANT: Davis, Stephen R.
 ; TITLE OF INVENTION: Compositions Isolated from Bovine
 ; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
 ; FILE REFERENCE: 11000.1068
 ; CURRENT APPLICATION NUMBER: US/10/079,754A
 ; PRIOR FILING DATE: 2002-02-19
 ; CURRENT APPLICATION NUMBER: US 09/699,146
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US 60,162,701
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: US 09/644,190
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: US 60,150,330
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 585
 ; TYPE: DNA
 ; ORGANISM: Bovine
 US-10-079-754A-2

Query Match

74.2%; Score 448.2; DB 14; Length 585;

Best Local Similarity 99.3%; Pred. No. 1.9e-92;
 Matches 450; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 138 CTGACTCCCAACAAATATGAAGATCTTTTATCTTTGCTTCTTATATGCTCTCATCTAGC 197
 DB 133 CAGGACTCCCAACAAATATGAAGATCTTTTATCTTTTCTTATCTTCTTATGCTCTCATCTAGC 192

	Query Match	39.5%;	Score 238.4;	DB 14;	Length 267;
	Best Local Similarity	99.6%;	Pred. No. 1.2e-44;		
	Matches 239;	Conservative	0;	Mismatches 1;	Indels 0;
					Gaps 0;
Qy	138	CTGGACCTCCACCAATATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTTAGC	197		
Db	28	CAGGACCTCCACCAANTATGAAGATCTTTATCTTTGTCTTCATTATGGCTCTCATCCTTAGC	87		
Qy	198	CATGATTAGAGCTGATTTCATCTGAAGAGAGAAACGTCACAGGAAACGGAAAAACAATCATAG	257		
Db	88	CATGATTAGAGCTGATTTCATCTGAAGAGAGAAACGTCACAGGAAACGGAAAAACAATCATAG	147		
Qy	258	AGGATATTTTCAACAAATACAGCCCATATCAACGATATCCACTAAATTCCTCTCTGGGTA	317		
Db	148	AGGATATTTTCAACAAATACAGCCCATATCAACGATATCCACTAAATTCCTCTCTGGGTA	207		

Qy 318 TCATTTCCCTTAAATGCTGTAGTAACTACAGCACATGATTAGAGAGATTTTTCACAA 377
|||
Db 208 TCATTTCCCTTAAATGCTGTAGTAACTACAGCACATGATTAGAGAGATTTTTCACAA 267

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RESULT 6
US-10-079-623-200
/ Sequence 200, Application US/10079623
/ Publication No. US20020169302A1
/ GENERAL INFORMATION:
/ APPLICANT: Havukkala, Ilkka J.
/ APPLICANT: Glenn, Matthew
/ APPLICANT: Grigor, Murray R.
/ APPLICANT: Molenaar, Adrian J.
/ TITLE OF INVENTION: Compositions isolated from bovine
/ TITLE OF INVENTION: mammary gland and methods for their use.
/ FILE REFERENCE: 11000.1044c3
/ CURRENT APPLICATION NUMBER: US/10/079,623
/ CURRENT FILING DATE: 2002-02-19
/ NUMBER OF SEQ ID NOS: 370
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 200
/ LENGTH: 267
/ TYPE: DNA
/ ORGANISM: Bovine
US-10-079-623-200

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RESULT 7
US-10-079-754A-3
; Sequence 3, Application US/10079754A
; Publication NO. US20020164625A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Bovine
US-10-079-754A-3

Query Match          19.0%; Score 115; DB 14; Length 869;
Best Local Similarity 92.4%; Pred. No. 3.3e-16;
Matches 121; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      138 CTGGACTCCACCAATATGAAGATCTTTATCTTTCTTCATTATGGCTCTCATCTTAGC 197
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      56 CAGGACTCCACCAATATGAAGATCTTTATCTTTCTTCATTATGGCTCTCATCTTAGC 115

QY      198 CATGATTAGAGCTGATTTCATCTCAAGAGAAAGCTCACAGGAAACGGAACCAATCATAG 257
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      116 CATGATTAGAGCTGATTTCATCTGAAGAGAAAGCTCACAGGAAACGGAACCAATCATGT 175

QY      258 AGGATATTTTC 268

Db      176 ATGATTTCCTC 186

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RESULT 8
US-10-079-754A-5
; Sequence 5, Application US/10079754A
; Publication No. US2002016425A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R. J.
; APPLICANT: Molenaar, Adrian J.
; APPLICANT: Davis, Stephen R.
; TITLE OF INVENTION: Compositions Isolated from Bovine
; TITLE OF INVENTION: Mammary Gland and Methods for Their Use
; FILE REFERENCE: 11000.1068
; CURRENT APPLICATION NUMBER: US/10/079,754A
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/699,146
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60,162,701
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/644,190
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60,150,330
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Bovine
; US-10-079-754A-5

Query Match      14.4%; Score 87; DB 14; Length 96;
Best Local Similarity 94.7%; Pred. No. 2.8e-10;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      255 TTTCAACAATACGAGCCATATCAACGATATCCACTAAATATCCTCCTCGGTATCCATTT 324
Db      1 TTTCAACAATACGAGCCATATCAACGATATCCACTAAATATCCTCCTCGGTATCCATTA 60

QY      325 CCTTAAATGCTGTTTAGTAACACGAGCATGAT 359
Db      61 TCTTAAATGCTGTTTACCAACTACAGGCATGAT 95

RESULT 9
US-09-992-600A-5
; Sequence 5, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki

```

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992.600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
; US-09-992-600A-5

Query Match 11.7%; Score 70.4; DB 10; Length 438;
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTTCATCTTTTCATGACTGGACTCCACCAAAATGAGATCTTTATCTTTGCTTCAT 179
DB 50 GACTCTCTCTTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGCTTTGCTTTAGT 109
QY 180 TATGCTCTCTCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
DB 110 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 169
QY 240 ACGGAAAAAACATCAT 255
DB 170 TAGAGAAAATTCAT 185

US-09-992-600A-5

RESULT 10
US-09-924-340-5
; Sequence 5, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
; US-09-992-600A-5

; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
; US-09-924-340-5

Query Match 11.7%; Score 70.4; DB 10; Length 438;
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTTCATCTTTTCATGACTGGACTCCACCAAAATGAGATCTTTATCTTTGCTTCAT 179
DB 50 GACTCTCTCTTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTTGCTTTGCTTTAGT 109
QY 180 TATGCTCTCTCCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
DB 110 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 169
QY 240 ACGGAAAAAACATCAT 255
DB 170 TAGAGAAAATTCAT 185

US-09-992-095B-5

RESULT 11
US-09-992-095B-5
; Sequence 5, Application US/09992095B
; Publication No. US20030157485A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US5.DIV
; CURRENT APPLICATION NUMBER: US/09/992,095B
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
; US-09-924-340-5

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/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 318..438
/ FEATURE:
/ NAME/KEY: polyA signal
/ LOCATION: 397..402
/ FEATURE:
/ NAME/KEY: polyA site
/ LOCATION: 423..438
US-09-992-095B-5

Query Match      11.7%; Score 70.4; DB 10; Length 438;
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTCATCTTTTCATGACTGGACTCCACCAAAATATGAAGATCTTTATCTTTGCTTCAT 179
Db 50 GACTCTCTCTTGAAGTAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTGCTTTAGT 109
QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239
Db 110 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 169
QY 240 ACGGAAAAAACATCAT 255
Db 170 TAGAAGAAAAATTCAT 185

RESULT 13
US-10-000-489-5
; Sequence 5, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000.489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 5
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..83
; NAME/KEY: CDS
; LOCATION: 84..317
; NAME/KEY: 3'UTR
; LOCATION: 318..438
; NAME/KEY: polyA signal
; LOCATION: 397..402
; NAME/KEY: polyA site
; LOCATION: 423..438
US-10-000-489-5

Query Match      11.7%; Score 70.4; DB 15; Length 438;
Best Local Similarity 69.9%; Pred. No. 3.6e-06;
Matches 95; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 120 GAATTCATCTTTTCATGACTGGACTCCACCAAAATATGAAGATCTTTATCTTTGCTTCAT 179
Db 50 GACTCTCTCTTGAAGTAAAGGACTCAGCCAACTATGAAGTTTTTTTGTCTTTGCTTTAGT 109
QY 180 TATGGCTCTCATCTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239
Db 110 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 169
QY 240 ACGGAAAAAACATCAT 255
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Job time : 391 secs

RESULT 15
US-10-154-678-5
; Sequence 5, Application US/10154678
; Publication No. US20030162186A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: randaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 182.US1.REG
; CURRENT APPLICATION NUMBER: US/10/154-678

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 07:37:23 ; Search time 2272 Seconds
(without alignments)
7938.713 Million cell updates/sec

Title: US-10-079-754A-4
Perfect score: 604
Sequence: 1 gaagattttcagttctata.....tatcaagcataaaaaaaa 604

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
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24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82.2	13.6	553	14	CB985810
2	78.6	13.0	546	14	CB957544
3	78.6	13.0	555	14	CB986888
4	78.6	13.0	792	14	CB958289

5	78.6	13.0	793	14	CB984475
6	78.6	13.0	831	14	CB985521
7	78.6	13.0	929	14	CB987745
8	77.6	12.8	583	13	CB985825
9	77.6	12.8	622	13	CB985714
10	77.6	12.8	773	14	CB987175
11	77	12.7	312	9	AA376700
12	77	12.7	327	9	AA382524
13	77	12.7	330	9	AA376704
14	77	12.7	348	9	AA376689
15	77	12.7	390	13	CB983872
16	77	12.7	527	14	CB986478
17	77	12.7	533	14	CB985159
18	77	12.7	540	14	CB985785
19	77	12.7	543	14	CB985823
20	77	12.7	543	14	CB987834
21	77	12.7	544	14	CB987223
22	77	12.7	544	14	CB959166
23	77	12.7	545	14	CB985845
24	77	12.7	545	14	CB959029
25	77	12.7	546	14	CB956307
26	77	12.7	546	14	CB956449
27	77	12.7	546	14	CB957121
28	77	12.7	546	14	CB957972
29	77	12.7	546	14	CB985184
30	77	12.7	546	14	CB986281
31	77	12.7	546	14	CB986417
32	77	12.7	546	14	CB987123
33	77	12.7	546	14	CB987595
34	77	12.7	547	14	CB955720
35	77	12.7	547	14	CB956188
36	77	12.7	547	14	CB956487
37	77	12.7	547	14	CB956536
38	77	12.7	547	14	CB956860
39	77	12.7	547	14	CB956877
40	77	12.7	547	14	CB957224
41	77	12.7	547	14	CB957280
42	77	12.7	547	14	CB957414
43	77	12.7	547	14	CB957440
44	77	12.7	547	14	CB957523
45	77	12.7	547	14	CB957940

ALIGNMENTS

RESULT 1
CB985810
LOCUS
DEFINITION
IMAGE:30329983 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CB985810 553 bp mRNA linear EST 01-MAY-2003
AGENCOURT 13647469 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30329983 5', mRNA sequence.

CB985810
CB985810.1 GI:30280334
EST.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 553)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM143 row: b column: 08

High quality sequence stop: 553.

FEATURES
source

Location/Qualifiers
1. .553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:30329983"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: Sfil (ggccatagcc); Site_2: Sfil (ggcgctcgcc); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 Kb (range 0.60-3.5 Kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.6%; Score 82.2; DB 14; Length 553;
Best Local Similarity 62.8%; Pred. No. 0.00043;
Matches 145; Conservative 0; Mismatches 83; Indels 3; Gaps 1;
QY 140 GGACTCCACCAATATGAAGATCTTTATCTTTGCTTCATTATGGCTCTCATCTAGCCA 199
DB 62 GAACCCACCAACTATGAAGTCTCTCTTTCCTTCATCTTGGCTCTCATCTAGTTCCA 121
QY 200 TGATTAGAGCTGATTCATCTGAAGAGAAAGCTCAGAGAAACGGAACCAACATCATAGAG 259
DB 122 TGATTGGAGCTGATTCATCTCAGAGAGAAATTTTGGCTAGAAATGGAAGATTCGGTTATG 181
QY 260 GATATTTTCAACATACACGACCATATCAAGCATATCCACTAAATTTATCTCTCGGTATC 319
DB 182 GGTA---TGGCCCTATACGCCAGTTCAGACAAACCATATACCCACCAACATACCAAC 238
QY 320 CATTTCTTAAATGCTGCTTAGTACTACAGACATGATTAGAGATTT 370
DB 239 AATATACCTTTAATATCATCATGTAACCTGCAGGACATGATTATTAGGCTT 289

RESULT 2

CB957544 546 bp mRNA linear EST 29-APR-2003
LOCUS
DEFINITION
AGENCOURT_13785762 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30352504 5', mRNA sequence.
CB957544
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 546)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbe-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDCM151 row: 1 column: 17
High quality sequence stop: 546.
Location/Qualifiers
1. .546

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:30352504"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: Sfil (ggccatagcc); Site_2: Sfil (ggcgctcgcc); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 Kb (range 0.60-3.5 Kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.0%; Score 78.6; DB 14; Length 546;
Best Local Similarity 60.2%; Pred. No. 0.0017;
Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
QY 120 GAATTTTCATCTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTTGTTTCAT 179
DB 41 GACTCTCTCTTTCAGTAAAGGACTCAGCCAACTATGAAGTCTTTGTCTTTGCTTTAGT 100
QY 180 TATGGCTTCATCTAGCCATGATTAGAGCTCATCTCATCTGAAGAGAAACGTCACAGGAA 239
DB 101 CTGGCTCTCATGATTTCCATGATAGCGCTGATTCATGATGAAGAGACATCATGGTA 160
QY 240 ACGAAACCAACATCATAGAGGATATTTTCAACATACCGCCATATCAACGATATCCACT 299
DB 161 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCGAATTTCCATTTATGG 214
QY 300 AATATTCTCTCGCGTATCCATTCTTAAATGCTGCTTAGTAACATACAGGACATGAT 359
DB 215 GGACTATGATCAATATTCTATATGACATTTGATATCTTAGTATCATCGGCGATGAT 274
QY 360 TAGAGAGATTT 370
DB 275 TATAGAGGTTT 285

RESULT 3

CB986888 555 bp mRNA linear EST 01-MAY-2003
LOCUS
DEFINITION
AGENCOURT_13650592 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:30329446 5', mRNA sequence.
CB986888
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 555)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: NDCM141 row: k column: 23
High quality sequence stop: 551.

FEATURES

source Location/Qualifiers
 1. .555
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="IMAGE:30329446"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattggcc); Site 2: SfiI (ggccgctggcc); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.0%; Score 78.6; DB 14; Length 555;
 Best Local Similarity 60.2%; Pred. No. 0.0016;
 Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTTCATGACTGGACTCCACCATAATATGAAGATCTTTATCTTTGTCTTCAT 179
 Db 41 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTITGCTTTGCTTTAGT 100
 QY 180 TATGGCTCTCATCCTAGCCTAGCATGATTAGACTGATTCATCTGAAGAGAAACGTCACAGAA 239
 Db 101 CTGGCTCTCATGATTTCATGATTAGCGCTGATTCACATGAAGAAAGACATCATGGGTA 160
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACACAGCCATATCAACGATATCCACT 299
 Db 161 TAGAGAAATTCAT-----GAAAGCATCATTCACATCGAGATTCTCCATTTATGG 214
 QY 300 AAATATATCTCTGCGTATCCATTTCTTAAATGCTGTTAGTAGTAACATACAGGACATGAT 359
 Db 215 GGACTATGGACCAAAATTATCTATATGACAAATTGATATCCTTAGTATATCATGGGGCATGAT 274
 QY 360 TAGAGAGATTT 370
 Db 275 TATAGAGGTTT 285

RESULT 4

CB958289
 LOCUS CB958289 792 bp mRNA linear EST 29-APR-2003
 DEFINITION AGENCOURT 13778124 NIH MGC_184 Homo sapiens cDNA clone
 IMAGE:30352112 5', mRNA sequence.
 ACCESSION CB958289
 VERSION CB958289.1 GI:30214405
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 792)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: http://image.llnl.gov

FEATURES

source Location/Qualifiers
 1. .792
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:30352112"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattggcc); Site 2: SfiI (ggccgctggcc); Library is oligo-dr primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.0%; Score 78.6; DB 14; Length 792;
 Best Local Similarity 60.2%; Pred. No. 0.0014;
 Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTTCATGACTGGACTCCACCATAATATGAAGATCTTTATCTTTGTCTTCAT 179
 Db 40 GACTCTCCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTITGCTTTGCTTTAGT 99
 QY 180 TATGGCTCTCATCCTAGCCTAGCATGATTAGACTGATTCATCTGAAGAGAAACGTCACAGAA 239
 Db 100 CTGGCTCTCATGATTTCATGATTAGCGCTGATTCACATGAAGAAAGACATCATGGGTA 159
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACACAGCCATATCAAGATATCCACT 299
 Db 160 TAGAGAAATTCATCGATAAAAA-----CATCATTCACATCGAGATTTCATTTATGG 213
 QY 300 AAATATATCTCTCTGCGTATCCATTTCTTAAATGCTGTTAGTAGTAACATACAGGACATGAT 359
 Db 214 GGACTATGGATCAAAATTATCTATATGACAAATTGATATCCTTAGTATATCATGGGGCATGAT 273
 QY 360 TAGAGAGATTT 370
 Db 274 TATAGAGGTTT 284

RESULT 5

CB984475
 LOCUS CB984475 793 bp mRNA linear EST 01-MAY-2003
 DEFINITION AGENCOURT 13459298 NIH MGC_184 Homo sapiens cDNA clone
 IMAGE:30327061 5', mRNA sequence.
 ACCESSION CB984475
 VERSION CB984475.1 GI:30278999
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 1 (bases 1 to 793)
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: http://image.llnl.gov

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM135 row: h column: 14
 High quality sequence stop: 486.
 Location/Qualifiers

FEATURES

1. 793
 Location/Qualifiers

source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone="IMAGE:30327061"
 /clone_lib="NIH_MGC_184"
 /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggcattatggcc); Site_2: SfiI (ggcgcctggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.0%; Score 78.6; DB 14; Length 793;
 Best Local Similarity 60.2%; Pred. No. 0.0014;
 Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
 QY 120 GAATTCATCTTCATGACTGGACTCCACCAATATGAGATCTTTATCTTGTCTTCAT 179
 Db 41 GACTCTCTCTTGAGTAAAGGACTCAGCCAATATGAAGTTTTTGTCTTGTCTTAGT 100
 QY 180 TATGGCTCTCATCTGACCATGATTAGAGCTGATTCTGTAAGAGAAACGTCACAGGAA 239
 Db 101 CTGGCTCTCATGATTTCATGATTAGCGTGATTCACATGAAGAAAGACATCATGGGTA 160
 QY 240 ACGGAAACATCATAGAGGATATTTCAACATACCGCATACAGCATATCCACT 299
 Db 161 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCCAGATTTCCATTTATGG 214
 QY 300 AAATTATCTCTCGTGATTCATTTCTTAAATGCTGTAGTAATACTACAGGACATGAT 359
 Db 215 GGACTATGGATCAATATCTATATGACAAATTGATATCTTAGTATATCATGGGCATGAT 274
 QY 360 TAGAGAGATTT 370
 Db 275 TATAGAGGTTT 285

RESULT 6
 CB985521
 LOCUS
 DEFINITION
 AGENCOURT_13652179 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30327061 5', mRNA sequence.
 ACCESSION
 CB985521
 VERSION
 CB985521.1 GI:30280045
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 831)
 AUTHORS
 NIH-MGC <http://imgc.ncbi.nih.gov/>.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM136 row: m column: 02
 High quality sequence stop: 177.
 Location/Qualifiers

1. 831
 Location/Qualifiers

source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30327553"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggcattatggcc); Site_2: SfiI (ggcgcctggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 13.0%; Score 78.6; DB 14; Length 831;
 Best Local Similarity 60.2%; Pred. No. 0.0013;
 Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
 QY 120 GAATTCATCTTCATGACTGGACTCCACCAATATGAGATCTTTATCTTGTCTTCAT 179
 Db 41 GACTCTCTCTTGAGTAAAGGACTCAGCCAATATGAAGTTTTTGTCTTGTCTTAGT 100
 QY 180 TATGGCTCTCATCTGACCATGATTAGAGCTGATTCTGTAAGAGAAACGTCACAGGAA 239
 Db 101 CTGGCTCTCATGATTTCATGATTAGCGTGATTCACATGAAGAAAGACATCATGGTA 160
 QY 240 ACGGAAACATCATAGAGGATATTTCAACATACCGCATATCAACATATCCACT 299
 Db 161 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCCAGATTTCCATTTATGG 214
 QY 300 AAATTATCTCTCGTGATTCATTTCTTAAATGCTGTAGTAATACTACAGGACATGAT 359
 Db 215 GGACTATGGATCAATATCTATATGACAAATTGATATCTTAGTATATCATGGGCATGAT 274
 QY 360 TAGAGAGATTT 370
 Db 275 TATAGAGGTTT 285

RESULT 7
 CB987745
 LOCUS
 DEFINITION
 AGENCOURT_13631497 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30327757 5', mRNA sequence.
 ACCESSION
 CB987745
 VERSION
 CB987745.1 GI:30282265
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 929)
 AUTHORS
 NIH-MGC <http://imgc.ncbi.nih.gov/>.
 TITLE
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDCM137 row: e column: 14
 High quality sequence stop: 386.

FEATURES

Location/Qualifiers
 1..929
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30327757"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 184"
 /note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccatgggc); Site_2: SfiI (ggccctgggc); SfiI (ggccatgggc); Site_2: SfiI (ggccctgggc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 13.0%; Score 78.6; DB 14; Length 929;
 Best Local Similarity 60.2%; Pred. No. 0.0013;
 Matches 151; Conservative 0; Mismatches 94; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
 Db 21 GACTCTCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTGTCTTTGCTTTAGT 80
 QY 180 TATGGCTCTCATCTAGCATGATTTAGAGCTGATTCATCTGAAGAGAAACGTACAGGAA 239
 Db 81 CTTGGCTCTCATCTTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 140
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACAGCCATATCAACGATATCCACT 299
 Db 141 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCGAGATTTCCATTTATGG 194
 QY 300 AAATTATCCTCTGGCTATCCATTTCTTAAATGCTTGTAGTAACTACAGGACATGAT 359
 Db 195 GGACTATGGATCAAAATTACTATATGCAATGATATCCTTAGTAACTATGATGCGGCATGAT 254
 QY 360 TAGAGAGATTT 370
 Db 255 TATAGAGGTTT 265

RESULT 8
 BX485825 583 bp mRNA linear EST 04-SEP-2003
 LOCUS DXFP268L09248_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DXFP268L09248 5', mRNA sequence.
 ACCESSION BX485825
 VERSION BX485825.1 GI:31948944
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 583)
 Othenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
 Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
 EST (Othenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
 et al.)

JOURNAL COMMENT

Unpublished (2003)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No s1 sequence
 available.

This clone (DXFP268L09248) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
 1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DXFP268L09248"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlcc3)"
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN

Query Match 12.8%; Score 77.6; DB 13; Length 583;
 Best Local Similarity 56.2%; Pred. No. 0.0023;
 Matches 189; Conservative 0; Mismatches 139; Indels 8; Gaps 2;
 QY 120 GAATTTTCATCTTTTCATGACTGGACTCCACCAATATGAAGATCTTTATCTTTGCTTCAT 179
 Db 38 GACTCTCTCTTGAGTAAAGGACTCAGCCAACTATGAAGTTTTTGTCTTTGCTTTAGT 97
 QY 180 TATGGCTCTCATCTAGCATGATTTAGAGCTGATTCATCTGAAGAGAAACGTACAGGAA 239
 Db 98 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGGTA 157
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACAGCCATATCAACGATATCCACT 299
 Db 158 TAGAAGAAATTCAT-----GAAAGCATCATTCACATCGAGATTTCCATTTATGG 211
 QY 300 AAATTATCCTCTGGCTATCCATTTCTTAAATGCTTGTAGTAACTACAGGACATGAT 359
 Db 212 GGACTATGGATCAAAATTACTATATGCAATGATATCCTTAGTAACTATGATGCGGCATGAT 271
 QY 360 TAGAGAGATTTTTCACAAATGATTTTCTCTACTCTTTCTGTGTGTGTTGTTGAAAACCATCTTTC 419
 Db 272 TATAGAG--GTAAGCTGACTCTAGTGTCTTTCTTTCTAGAGAGTGTCAACACTGACAGTT 329
 QY 420 AAATGAATATAAAACAAAGAAAAAAATCAGTCAAGT 455
 Db 330 TAAAAAAAAGCCATAGCTACACCATTCAGT 365

RESULT 9
 BX485714 622 bp mRNA linear EST 04-SEP-2003
 LOCUS DXFP268L09248_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DXFP268L09248 5', mRNA sequence.
 ACCESSION BX485714
 VERSION BX485714.1 GI:31948727
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 622)
 Othenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
 Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
 EST (Othenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
 et al.)
 JOURNAL Unpublished (2003)

COMMENT

Contact: MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No sl sequence
 available.
 This clone (DKFZp686E20248) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clones@rzpd.de.
 Location/Qualifiers

FEATURES

source

1. 622
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686E20248"
 /dev_stages="adult"
 /lab_host="DH10B"
 /clone_lib="686" (synonym: hlcc3)
 /note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN

Query Match 12.8%; Score 77.6; DB 13; Length 622;
 Best Local Similarity 56.2%; Pred. No. 0.0023;
 Matches 189; Conservative 0; Mismatches 139; Indels 8; Gaps 2;
 QY 120 GAATTTTCATCTTTCATGACTGCTCCACCAATATGAGATCTTTATCTTCTTCAT 179
 Db 36 GACTCTCTCTTGAGTAAAGACTCAGCCACTGATGAGTTTTCCTTTCTTTAGT 95
 QY 180 TATGCTCTCATCTAGCCATGATTTAGAGTGTATTCATCTGAGAGAAACGTCACAGGAA 239
 Db 96 CTGGCTCTCATGATTTCCATGATTTAGCGTGTATTCACATGAAAGAGACATCATGGGTA 155
 QY 240 ACGGAAACACATCATAGAGGATATTTTCAACATACCGCCATATCAACGATATCCACT 299
 Db 156 TAGAGAAATTCAT-----GNAAGCATCATTCACATCGAGATTTCCATTTATGG 209
 QY 300 AAATATCTCTCTCGGTATCCATTCCTTAAAGTGTCTAGTAACTACAGGACATGAT 359
 Db 210 GGACTATGGATCAAAATATCTATATGACAATTCATATCTTCTAGTAACTATCGGGCATGAT 269
 QY 360 TAGAGAGATTTTTCACATGATTTTCTCTACTCTTTCTGTGTGTTGAAACCATCTTTC 419
 Db 270 TATAGAG--GTAAGCTGACTCTAGTACTTCTTCTCTTCTAGAGTGTCAACATGACGTT 327
 QY 420 AAATGAATTAACAAAGAAAGAAAGAAATTCAGTCAAGT 455
 Db 328 TAAAAAAGGCAATGCTAAGCTAACACCACTTCAGT 363

RESULT 10

CB987175
 LOCUS CB987175
 DEFINITION AGNCOURT_13650773 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30329891 5', mRNA sequence.
 CB987175
 VERSION CB987175.1 GI:30281695
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 773)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 AUTHORS Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovics

cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov

Plate: NDCM142 row: n column: 12
 High quality sequence stop: 181.
 Location/Qualifiers

FEATURES

source

1. 773
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30329891"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
 SfiI (ggccattggcc); Site_2: SfiI (ggccctggcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGGCGCATATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)EN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.8%; Score 77.6; DB 14; Length 773;
 Best Local Similarity 59.8%; Pred. No. 0.002;
 Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTCATGACTGCTCCACCAATATGAGATCTTTATCTTCTTCAT 179
 Db 41 GACTCTCTCTTGAGTAAAGACTCAGCCACTGATGAGTTTTCCTTTCTTTAGT 100
 QY 180 TATGCTCTCATCTAGCCATGATTTAGAGTGTATTCATCTGAGAGAAACGTCACAGGAA 239
 Db 101 CTGGCTCTCATGATTTCCATGATTTAGCGTGTATTCACATGAAAGAGACATCATGGGTA 160
 QY 240 ACGGAAACACATCATAGAGGATATTTTCAACATACCGCCATATCAACGATATCCACT 299
 Db 161 TAGAGAAATTCAT-----GNAAGCATCATTCACATCGAGATTTCCATTTATGG 214
 QY 300 AAATATCTCTCTCGGTATCCATTCCTTAAAGTGTCTAGTAACTACAGGACATGAT 359
 Db 215 GGACTATGGATCAAAATATCTATATGACAATTCATCTTATAGTAACTATCGGGCATGAT 274
 QY 360 TAGAGAGATTT 370
 Db 275 TATAGAGTTT 285

RESULT 11

AA376700
 LOCUS AA376700
 DEFINITION EST89157 Salivary gland Homo sapiens cDNA 5' end similar to
 histatin 1, mRNA sequence.
 AA376700
 VERSION AA376700.1 GI:2029018
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 312)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
 Clayton, R.A., Cline, R.R., Cotton, M.D., Earle-Rhughes, J., Fine, L.D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

7566098

Other ESTs: EST89156 THC102726

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

source

1. .312

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="ATCC (inhost):181117"

/db_xref="taxon:9606"

/dev_stage="adult"

/clone_lib="Salivary gland"

/note="Organ: salivary gland; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 12.7%; Score 77; DB 9; Length 312;

Best Local Similarity 59.8%; Pred. No. 0.004;

Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 120 GAATTTTCATCTTCATGACCTGACCTCCACCAATATGAGATCTTTATCTTGTCTTCAT 179

Db 12 GACTCTCTCTTTCAGTAAAGAGACTGAGCAACTATGAGTTTGTCTTGTCTTAGT 71

QY 180 TATGCTCTCATCTTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239

Db 72 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGTA 131

QY 240 ACGGAAACACATCATAGAGGATATTTTCAACATACAGCCATCATCAACGATATCCACT 299

Db 132 TAGAGAAATTCAT-----GAAAGCATCATTCACATCAGAAATTCATTTATGG 185

QY 300 AAATATCTCTCGCTGCTATCCATTTCTTTAAATGCTGTTAGTAACATACAGGACATGAT 359

Db 186 GGACTATGGATCAAAATTAATCTATATGACAATTTGATATCCTTAGTAATCATGGGCATGAT 245

QY 360 TAGAGAGATTT 370

Db 246 TATAGAGGTTT 256

RESULT 12

AA382524

LOCUS

EST95743 Testis I Homo sapiens cDNA 5' end similar to histatin 1,

DEFINITION

mRNA sequence.

ACCESSION

AA382524

AA382524.1 GI:2034842

VERSION

EST.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 327)

REFERENCE

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,

He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,

Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,

Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,

Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

7566098

Other ESTs: THC102726

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1. .327

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="ATCC (inhost):186803"

/db_xref="taxon:9606"

/sex="male"

/dev_stage="adult"

/clone_lib="Testis I"

/note="Organ: testis; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

Query Match 12.7%; Score 77; DB 9; Length 327;

Best Local Similarity 59.8%; Pred. No. 0.0039;

Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;

QY 120 GAATTTTCATCTTCATGACCTGACCTCCACCAATATGAGATCTTTATCTTGTCTTCAT 179

Db 24 GACTCTCTCTTTCAGTAAAGAGACTGAGCAACTATGAGTTTGTCTTGTCTTAGT 83

QY 180 TATGCTCTCATCTTAGCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGAA 239

Db 84 CTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAGAGACATCATGGTA 143

QY 240 ACGGAAACACATCATAGAGGATATTTTCAACATACAGCCATCATCAACGATATCCACT 299

Db 144 TAGAGAAATTCAT-----GAAAGCATCATTCACATCGAGAAATTCATTTATGG 197

QY 300 AAATATCTCTCGCTGCTATCCATTTCTTTAAATGCTGTTAGTAACATACAGGACATGAT 359

Db 198 GGACTATGGATCAAAATTAATCTATATGACAATTTGATATCCTTAGTAATCATGGGCATGAT 257

QY	360	TTAGAGAGATT 370	AA376704	330 bp	mRNA	linear	EST 21-APR-1997
Db	258	TATAGAGGTTT 268	AA376704	330 bp	mRNA	linear	EST 21-APR-1997
QY	180	TATGGCTCTCCTAGCCATGATTAGAGCTGATTTCATCTGAAGAGAAACGTCACAGGAA	239	348 bp	mRNA	linear	EST 21-APR-1997
Db	76	CTTGGCTCTCCTAGCATGTTCCATGATTAGCGCTGATTTCATGATGAAGAAGACATCATGGGTA	135	348 bp	mRNA	linear	EST 21-APR-1997
QY	240	ACGAAAAAATCATATAGAGGATATTTTCAACAATACCAGCCATATCAACGATATCCACT	299	348 bp	mRNA	linear	EST 21-APR-1997
Db	136	TAGAAGAAATTCAT-----GAAAAGCATCATTCACATCGAGAAATTTCCATTTTATGG	189	348 bp	mRNA	linear	EST 21-APR-1997
QY	300	AAATATCTCTCTGGGTATTCATTCCTTAAATCTGCTTAGTAACTACAGGACATGAT	359	348 bp	mRNA	linear	EST 21-APR-1997
Db	190	GGCATATGATCAAAATATATCTATATGACAATTCATCTTAGTAACTATCGGGCATGAT	249	348 bp	mRNA	linear	EST 21-APR-1997
QY	360	TTAGAGAGATT 370	AA376704	330 bp	mRNA	linear	EST 21-APR-1997
Db	250	TATAGAGGTTT 260	AA376704	330 bp	mRNA	linear	EST 21-APR-1997
RESULT 13							
LOCUS	AA376704						
DEFINITION	h1statin 1, mRNA sequence.						
ACCESSION	AA376704						
VERSION	AA376704.1						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 330)						
AUTHORS	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.						
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence						
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)						
MEDLINE	96026280						
PUBMED	7566098						
COMMENT	Other ESTs: EST89160 THC102726 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tcdb/hgi/hgi.html) Seq primer: M13 Reverse Location/Qualifiers 1. .330 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="ATCC (inhost):181119" /db_xref="taxon:9606" /dev_stage="adult" /clone_lib="Salivary gland" /note="Organ: salivary gland; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"						
FEATURES	source						
ORIGIN	12.7%; Score 77; DB 9; Length 330; Query Match 59.8%; Pred. No. 0.0038; Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;						
QY	120	GAATTTTCATCTTTCATGACCTGAGCTCCACCAATATGAGAGATCTTATCTTCTTCTTAT	179				
Db	16	GACTCTCTCTTGTAGTAAAGGACTCAGCCACTGAGAGTTTGTGCTTCTTCTTCTTCTT	75				

Site_1: EcoRI; Site_2: XhoI
 Query Match 12.7%; Score 77; DB 9; Length 348;
 Best Local Similarity 59.8%; Pred. No. 0.0038;
 Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTTCATGACTGACCTCCACCAATATGAAGATCTTTTATCTTTGTCTTCAT 179
 DB 12 GACTCTCCCTTTGAGTAAAGGACTCAGCCACTATGAAGTCTTTTGTCTTTGTCTTTAGT 71
 QY 180 TATGGCTTCATCCTTAGCCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
 DB 72 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 131
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACAGCCATATCAACGATATCCACT 299
 DB 132 TAGAAGAAATTCAT-----GAAAAGCATCATTCACATCCAGAAATTTCCATTTATGG 185
 QY 300 AAATTATCTCTCGCTGCTTCCATTTCTTTAAATGCTGCTTAGTAACTACAGGACATGAT 359
 DB 186 GGACTATGGATCAAAATATCTATATGACAATTGATATCTTAGTAATCATGGGGCATGAT 245
 QY 360 TAGAGAGATTT 370
 DB 246 TATAGAGGTTT 256
 RESULT 15
 BX283872
 LOCUS
 DEFINITION BX283872 NIH_MGC_81 Homo sapiens cDNA clone IMAGE958N191131 ;
 IMAGE:4289874, mRNA sequence.
 ACCESSION
 VERSION BX283872
 KEYWORDS EST.
 SOURCE BX283872.1 GI:28848326
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 390)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radelof, U., Schneider, D. and Korn, B.
 Human UnigeneSet - RZPD3
 Unpublished (2003)
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE958N191131.
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
 Human UnigeneSet - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/ClonCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 pCMV-M13u, Primer sequence: CGTTGTAACGACGCGCCAGT.
 Location/Qualifiers
 1..390
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE958N191131 ; IMAGE:4289874"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 81"
 /note="Organ: muscle (skeletal); Vector: pDNR-LIB
 (Clontech); Site: 1: SfiI (ggccgctcgcc); Site 2: SfiI
 (ggccatagggc); 5' and 3' adaptors were used in cloning
 as follows: 5'-CACGGCCATTATGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."
 ORIGIN
 Query Match 12.7%; Score 77; DB 13; Length 390;
 Best Local Similarity 59.8%; Pred. No. 0.0036;
 Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;
 QY 120 GAATTTTCATCTTTTCATGACTGACCTCCACCAATATGAAGATCTTTTATCTTTGTCTTCAT 179
 DB 35 GACTCTCTCTTTGAGTAAAGGACTCAGCCACTATGAAGTCTTTTGTCTTTGTCTTTAGT 94
 QY 180 TATGGCTTCATCCTTAGCCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
 DB 95 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 154
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACAGCCATATCAACGATATCCACT 299
 DB 155 TAGAAGAAATTCAT-----GAAAAGCATCATTCACATCGAGAAATTTCCATTTATGG 208
 QY 300 AAATTATCTCTCTCGCTGCTTCCATTTCTTTAAATGCTGCTTAGTAACTACAGGACATGAT 359
 DB 209 GGACTATGGATCAAAATATCTATATGACAATTGATATCTTAGTAATCATGGGGCATGAT 268
 QY 360 TAGAGAGATTT 370
 DB 269 TATAGAGGTTT 279

Search completed: August 16, 2004, 00:15:22
 Job time : 2275 secs

FEATURES
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 Alto, CA)."
 ORIGIN
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 Best Local Similarity 59.8%; Pred. No. 0.0038;
 Matches 150; Conservative 0; Mismatches 95; Indels 6; Gaps 1;
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 DB 12 GACTCTCCCTTTGAGTAAAGGACTCAGCCACTATGAAGTCTTTTGTCTTTGTCTTTAGT 71
 QY 180 TATGGCTTCATCCTTAGCCCATGATTAGAGCTGATTCATCTGAAGAGAAACGTCACAGGAA 239
 DB 72 CTTGGCTCTCATGATTTCCATGATTAGCGCTGATTCACATGAAAAGAGACATCATGGGTA 131
 QY 240 ACGGAAAAACATCATAGAGGATATTTTCAACAATACAGCCATATCAACGATATCCACT 299
 DB 132 TAGAAGAAATTCAT-----GAAAAGCATCATTCACATCCAGAAATTTCCATTTATGG 185
 QY 300 AAATTATCTCTCGCTGCTTCCATTTCTTTAAATGCTGCTTAGTAACTACAGGACATGAT 359
 DB 186 GGACTATGGATCAAAATATCTATATGACAATTGATATCTTAGTAATCATGGGGCATGAT 245
 QY 360 TAGAGAGATTT 370
 DB 246 TATAGAGGTTT 256

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